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Database :
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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              A_Geneseq_101002:*

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Gapop 10.0 , Gapext 0.5
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598
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): /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT: *
:/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					AAW06577;	AAW
	126 AA.		Protein;	standard;	06577	JLT 1 06577 AAW
	ALIGNMENTS					
Arabidopsis chaila		1	U	10.1		ť
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nan homo	AAU83013	23	888	13.2	٦,	42
A20	428	21	647	ω.	vo	4
Mutant A20 Binding	æ	21	647		79.5	
Mutant A20 Binding	AAY44286	21	647	ω.	9	39
Mutant A20 Binding	AAY44285	21	647		9	38
Murine A20 Binding	AAY44279	21	647	ω	9	37
Murine A20 Binding	AAY44280	21	594		9	36
Neisseria meningit	AAY74903	21	231	٠	80	ა 5
Drosophila melanog	ABB62191	22	1224	•	80.5	34
Neisseria meningit	AAY74906	21	232	13.5	•	33
Streptococcus poly	ABP29822	23	815	•	82	32
Streptococcus polv	ABP27680	23	815	13.7	82	31
Neisseria meningit	AAY74907	21	232		82	30
3	AAY74904	21	232		اھ	29
Ð	AAB69070	22	1374		82.5	28
Arabidopsis thalia	AAG51259	21	754		ν:	27
Arabidopsis thalia	AAG51260	21	638		2 !	26
Arabidonsis thalia	AAG51261	21	620		N !	25
Human protein sec	AAM79969	26	ν υ υ			2 4
Novel human diagno	ABG2422/	۲ ۲	1 0 V	12.9	o م) L
ש	AABZ8151	2 6	1530		ວິດ) F
protein isc	ABB72256	23	1529	•	87	20
Skin cell protein,	AAB56056	22	1529	٠		19
	AAY76117	21	1529	14.5		18
SI	AAB61239	22	1529	٠	88	17
length	AAW96702	20	1529	14.7		16
slit-	AAY27145	20	52	14.7		15
Slit	AAY17499	20	1525	14.7		14
Ę	670	20	50	14.7		
or ⊦	~) ·	20	50	14.7	ω.	۱ <u>۱</u> ا ۲
Listeria monocytog	ABB49111	2	688	17.3	103.5	1

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Transfer of at least 2 saccharide units using poly:glycosyl:transferase - isolated from N. gonorrhoeae, catalyses the addition of both GlcNac and GalNac di:saccharide(s) units to a
                                                                                                                                                                                                                                                                                   21-MAR-1997 (first entry)
                                           WPI; 1997-052351/05.
N-PSDB; AAT49230.
                                                                            Buczala SL,
                                                                                                                      07-JUN-1995;
                                                                                                                                           03-JUN-1996;
                                                                                                                                                                19-DEC-1996
                                                                                                                                                                                      WO9640971-A1.
                                                                                                                                                                                                         Neisseria gonorrhoeae ATCC 33084.
                                                                                                                                                                                                                             Polyglycosyltransferase; N-acetylglucosaminyl transferase; N-acetylgalactosaminyl transferase; lipo-oligosaccharide.
                                                                                                                                                                                                                                                             Lipo-oligosaccharide gene-encoded protein.
                                                                                                (NEOS-) NEOSE TECHNOLOGIES INC
                                                                            Johnson KF, Roth S;
                                                                                                                      95US-0478140.
                                                                                                                                           96WO-US08323.
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RESULT 2
ABB54412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A lipooligosaccharide-encoding gene region (AAT49230) of Neisseria gonorrhoeae ATCC 33084 includes coding sequences for 5 proteins (AAW06576-80), one of which (AAW06576) is a polyglycosyltransferase that catalyses the addition of Glona and Galnac disaccharides to a galactose molety. The function of the other 4 proteins is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single galactose moiety
                                                                         The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification nucleic acid sequence, particularly to identify Lactococcus lactis or
                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
             invention helps research in lactic bacteria, particularly useful in production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent paten
                                                    related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The
                                                                                                                                             Claim 6; SEQ ID No 1114; 2504pp; French
                                                                                                                                                                                                                                       Bolotine
                                                                                                                                                                                                                                                               (INRG )
                                                                                                                                                                                                                                                                                        11-APR-2000;
                                                                                                                                                                                                                                                                                                                 11-APR-2000;
                                                                                                                                                                                                                                                                                                                                           12-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                            Lactococcus lactis IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                    Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Lactococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB54412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB54412 standard; Protein;
    WO200177334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     galactose moiety. The fun
tated in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LQAYAYFKQLPEAAALAAANKRYQNLLKKADAALGEVNESLLQQDEEKALYAAAQGLQPK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match
                                                                                                                                                                     nucleotide sequence useful in tis and related species -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IALLGE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IAAAVAEGNFRTALSELASVKPQVDAFFDGVMVMAEDAAVKQNRLNLLNRLAEQMNAVAD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQAVAVFKQLPEAAALAAANKRVQNLLKKADAALGEVNESLLQQDEEKALYAAAQGLQPK
                                                                                                                                                                                                             2002-043418/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126;
                                                                                                                                                                                                                                                               INRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                            lactis protein
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  (published 18-OCT-2001) which is available in electronic
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                                                                                                                                                                                                                                        Sorokine
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Pred. No. 1.3e-55;
; Mismatches 0;
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                equivalent patent
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                                                                                                                                                                                      Lactococcus
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                                 The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 format directly from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU33401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU33401
                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                           WPI; 2001-611495/70
                                                                                                                                                                                                                                                                                                 Haselbeck R, Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                             27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200170955-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus
                                                                                                                                                                                               Example 3;
                                                                                                                                                                                                                                                                                                                                                                                                      23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAY-2000;
                         programmes. The antisense nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                       (ELIT-)
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  wide
                                                                                                                                                                                                                       polynucleotides for the identification and development ibiotics, comprise sequences of antisense nucleic acids
homologous nucleic acids which are required ide variety of organisms. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NILKKADAALGEVNESLLQQDEEKALYAAAQGLQPKIAAAVAEGNFRTALSELASVKPQV 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prokaryotic cellular
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2000US-207727P.
2000US-242578P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           faecalis cellular proliferation protein #37.
                                                                                                                                                                                                                                                                                                                                                                  2001US-269308P
                                                                                                                                                                                                                                                                                                                                                                              2000US-253625P
2000US-257931P
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                                                                                                                                                                                                                                                                                                   Ohlsen
Xu HH;
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                                                                                                                                                                                                                                                                                                               Zyskind JW,
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design.
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J. No. 9.6e-09;
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               for cell proliferation
                             is also useful to screen
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RESULT 4
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Best Local S
Matches 46
           This sequence represents the glycyl trNA synthetase (glyS) beta subunit from Streptcocccus pneumoniae 0100993 (NCIMB 40794). The polynucleotide encoding glyS can be used for the requiring glyS activity. Sequences antisense to treat conditions requiring glyS activity. Sequences antisense to the polynucleotide can be used to control glyS expression. GlyS, or glyS expressing vectors can be used to induce an immune response, i.e. an antibody (Ab) and/or T cell response, against S. pneumoniae to protect against infection, or to screen for antagonists or agonists of the polynucleotide encoding glyS or glyS's activity, i.e. antibacterials. The antagonist, e.g. an anti-glyS Ab, can used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form the printed specification, but was obtained in electronic format directly from WIPO at
treat conditions requiring glyS inhibition,
                                                                                                                                                                      Claim
                                                                                                                                                                                                          DNA encoding glycyl tRNA synthetase useful for diagnosis, treatment and
                                                                                                                                                                                                                                                                                                                         (SMIK )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycyl tRNA synthetase beta; glyS beta polypeptide; immune response; vaccine; antibacterial; meningitis; bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW33905 standard;
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46; Conser
                                                                                                                                                                                                                                                                                                                         SMITHKLINE SMITHKLINE
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                                                                                                                                                                    Page 40-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               989
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BEECHAM PLC.
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Pred. No.
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                                                                                                                                                                                                           of Streptococcus pneumoniae prevention of bacterial
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infection, particularly meningitis. A fragment of the polynucleotide encoding glyS can used as a probe to isolate full length or related sequences, or diagnose, e.g. by polymerase chain reaction, infection stage and type, including mutation and polymorphism detection. Diagnosis may also be achieved by detecting glyS gene overexpression, e.g. by immunoassay. The Ab can used to treat infection, isolate or identify glyS expressing clones, purify glyS and as an immunoassay reagent. More generally, the products can prevent adhesion of bacteria to wounds and in dwelling devices, block glyS protein mediated invasion of mammalian cells and block the normal progression of infection.
                                                                                                                                                                    WPI; 1998-321534/28
N-PSDB; AAV31656.
                                                                                                                                                                                                                                                                                                                                                                               Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                        Glycyl tRNA synthetase-beta gene; antagonist; antibacterial activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW37953 standard;
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                                                                                                                screening for antibacterial compounds,
                                                                                                                              polypeptides
                                                                                                                                                                                                          Lawlor EJ;
                                                                                                                                                                                                                                   (SMIK)
                                                                                                                                                                                                                                                                          18-APR-1997;
                                                                                                                                                                                                                                                                                                                            26-MAY-1998
                                                                                                                                                                                                                                                                                                                                                      US5756330-A
                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of glyS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VFKQLPEAAALAAANK-------RVQNLLKKADAALGEVNESLLQQDEEKALYAA 53
                                                                                                                                                                                                                                 SMITHKLINE SMITHKLINE
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                                                                                                                          pneumococcal glycyl tRNA synthetase subunit useful for producing recombinant polypept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                               pneumoniae
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                                                                                                                                                                                                                                   BEECHAM CORP.
BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
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35.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             (beta) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            678
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Pred. No. 2e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                     glys-beta; vaccine; agonist;
                                                                                                                and
                                                                                                                in DNA vaccines
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                                                                                                                             polypeptides
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This is the amino acid sequence of the Streptomyces pneumoniae nove glycyl tRNA synthetase-beta (glyS-beta) protein. The polynucleotid are useful for producing the recombinant polypeptides, which can be used in vaccines or to screen for glyS-beta or glyS-alpha agonists antagonists with potential antibacterial activity. The

protein. The polynucleotides polypeptides, which can be

Claim 1; Columns 7-8;

24pp; English

antagonists with potential antibacterial activity. polynucleotides are also useful for DNA vaccination

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RESULT 6
ABP26830
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24-NOV-2000;
07-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                               streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus spaniactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN65044-ABN1526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -  \frac{1}{2} \int_{\mathbb{R}^n} \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Telford J,
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antiinflammatory; infe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                    The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENO-)
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   as a vaccine or diagnostic
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2000GB-0028727.
2001GB-0005640.
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                                                                                                                                                                                                                                                                                                                                                                                relates to a protein (ABP25413-ABP30895) from group
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Pred. No. 2
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       composition.
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RESULT 7
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                                                                                                                                                                                                                                                                                                             27-OCT-2000;
24-NOV-2000;
07-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by
                                                                                                                                 New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein \dot{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus agalactiae
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DB; ABN67460.
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                                                                                                       Page 3435; 4525pp; English.
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2000GB-0028727.
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33.3%;
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                                                                                                                                                                                                                                             Margarit Ros YI,
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Pred. No. 1.1e-07;
5; Mismatches 37;
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RESULT 8
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streptococcus/GBS (Streptococcus agalactiae) or group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus/GAS (Streptococcus/GAS
                                                                                                                                                                                                                                                                                                                                                                                                                                               New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
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24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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Tettelin H;
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DB; ABN69437.
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                                                                                                                                                                                                                                                                                                                                                  English.
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.9e-07;
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Best Local
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                                                                                                                                                                               Novel human polypeptides and polynucleotides useful for diagnosing preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders -
                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; open reading frame; ORFX; gene therapy; cancer; hyperproliferative disorder; psoriasis; benign tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus proteins.
                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAY-2001; 2001WO-US10836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-DEC-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ORFX protein sequence SEQ ID NO:14812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUN-2002
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Pred. No. 1.1e-05;
8; Mismatches 41;
                                                                                                                       English.
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The present invention describes (referred to as open reading frain the specification). ABN15762

describes substantially purified human reading frame, ORFX, where X is 1-11491. ABN15762 to ABN27252 encode the human

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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treatin syndrome associated with ORFX-associated disorder. ORFX polynucleotide
                                                                                            Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequence from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   systemic cytokine damage
      Claim 5; SEQ ID NO
                                                                                                                                                                                                                            WPI; 2002-269010/31
                                                                                                                                                                                                                                                                                           Tietjen K,
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33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        given in ABP00010 to ABP11500. ORFX proteins are useful or preventing a pathology associated with an ORFX-associ
                                                                                                                                                                                                                                                                                           Weidler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
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   1799;
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   261pp +
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Pred. No. 1.4e-06;
Mismatches 32;
Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 23;
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                                                                                                                                acid sequences
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monocytogenes EGD-e (see ABA03041). The genome sequence and fragments it are useful for selecting probes and primers for detecting genes in monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins

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Best Local :
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                                                                                                                                         Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux J Bussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossari Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend J, Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L, Perez-Diaz J, Baguero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB49111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1018 MQL--VEPLED-FFNNVFVMVEEERVRKNRLALLNNIANLPKGVIDLSFL 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                            11-APR-2000; 2000FR-0004629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                      The present invention relates to the genome sequence of Listeria
                                                                                                  Claim 6;
                                                                                                                                                                                       WPI; 2002-010914/01.
                                                                                                                                                                                                                                                                                                                                                                                                       11-APR-2001; 2001WO-FR01118
                                                                                                                                                                                                                                                                                                                                                                                                                                    18-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200177335-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vitamin B12; bacterial infection; disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Listeria monocytogenes protein #1815
                                                                                                                                                                                                                                                                                                                                                (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    958 IVEAYSRPTRIVRGKDVGVGVEVLENAFETPQERTLWSTYTSIKDRIHTGIEIEDFTEIS 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 SELASVKPQVDAFFDGVMVMAEDAAVKQNRLNLLNRLAEQMNAVADIALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 LAAANKRVQNLLKKADAALG-EVNESLLQQDEEKALYAAAQGLQPKIAAAVAEGNFRTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32;
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                                                                                                  SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1067 AA;
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                                                                                                  ID No 1816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
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                                                                                               192pp;
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Pred. No. 0.
                                                                                                  French.
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                                                                                                                                                          for treatment
                                                                                                                                                                                                                                                           Durant L;
                                                                                                                                                                                                                                                                                                                     Dehoux P;
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Best Local 9
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                        vertebrate slit proteins encoding nucleic acid sequences have at least 60% homology to nucleic acid sequences AAX89161-163. The vertebrate-derived proteins can be produced recombinantly by transforming host cells with expression vectors comprising the encoding nucleic acids. The proteins of the invention are for diagnosing and treating cancer of the nerves, muscle and/or endocrine system.
                                                                                                                  The invention relates to a vertebrate-derived protein containing an amino acid sequence shown in AAY27137 and AAY27139. The vertebrate-derived protein has at least 55 % homology to one of sequences shown in AAY27141-Y27143, and has slit protein-like activity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication
                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                 New vertebrate slit protein - cancers in nerves, muscle and
                                                                                                                                                                                                                                                                                                                                                             05-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                          05-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP11164690-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vertebrate-derived protein; muscle; endocrine system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human slit-2 mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monocytogenes and related organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and modulate L. monocytogenes-related diseases. In addition, the generated and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections l
                                                                                                                                                                                                                                                                                                                              (ASAH ) ASAHI KASEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                 1999-411830/35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADLRTTIDAYFDNTLVMSDNDELKNNRLALLFELASFIKEFAQM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
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                                                                                                                                                                                                Page 43-47; 102pp; Japanese
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                                                                                                                                                                                                                                                                                                                                KOGYO KK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                slit protein; diagnosis; cancer; nerve;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1503
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                                                                                                                                                                                                                               useful for diagnosis and treatment endocrine system \,
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                                                                                                                                                                                                                                       The present sequence represents the mature protein sequence a slit-like polypeptide. The polypeptide is useful for the diagnosis and the treatment of all nervous diseases, thyroid
                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                         Claim 1; Page 17-21; 50pp; Japanese
                                                                                                                                                                                                                                                                                                                  New slit-like polypeptide - useful for diagnosis and nervous, thyroid, adrenal and muscular diseases  \begin{tabular}{ll} \hline \end{tabular} 
                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-161084/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Slit-like polypeptide; diagnosis; treatment; nervous disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Slit-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW96701 standard;
                                                                                                                                                                                                                                                                                                                                                                                (ASAH ) ASAHI KASEI KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thyroid disease;
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                       115 MNAVADIALLGE
                                                                                                 522 LEATGIFKKLPQLRKINFSNNKITDIEEGAFEGASGVNEILLTSNRLENVQHKMFKGLE- 580
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                                                                                                                         LQAVAVFKQLPEAAALAAANKRVQNLLKKADAALGEVNESLLQQDE-EKALYAAAQGLQP 59
FNCNCYLAWLGE
                                                                          KIAAAVAEGNFRTALSE-----LASVKPQVDAFFDGVMVMAEDAAVKQNRLNLLNRLAEQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FNCNCYLAWLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLKTLMLRSNRITCVGNDSFIGLSSVR-LLSLYDNQITTVAPGAFDTLHSLSTLNLLANP 639
                                                SLKTLMLRSNRITCVGNDSFIGLSSVR-LLSLYDNQITTVAPGAFDTLHSLSTLNLLANP 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIAAAVAEGNFRTALSE-----LASVKPQVDAFFDGVMVMAEDAAVKQNRLNLLNRLAEQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEATGIFKKLPQLRKINFSNNKITDIEEGAFEGASGVNEILLTSNRLENVQHKMFKGLE- 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                            adrenal diseases and muscular diseases
                                                                                                                                                                                                      1503 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adrenal disease; muscular disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                               14.7%;
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25.0%;
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                                                                                                                                                              Score 88;
Pred. No.
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Pred. No.
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                                                                                                                                                                          Length 1503;
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RESULT 14
AAX17499
IID AAX177499
IZ AAX177499
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AX AAX177
AX AAX17
AC AAX17

RESULT 15
AAY27145
ID AAY27
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                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the human Slit-1 protein. The present invention also describes a method for identifying agents which modulate the interaction of Robo and a Robo ligand comprising: combining a Robo golypeptide, a Slit polypeptide and a candidate agent under conditions where the Robo and Slit polypeptides normally (but for the presence of the agent) engage in a first interaction, where the Slit polypeptide specifically binds, activated or inhibits the activation of the Robo golypeptides in the presence of the agent, where a difference between the first and second interaction of the Robo and Slit polypeptides; and a second interaction of the Robo and Slit polypeptides; and a method to modulate the interaction of Robo and Slit polypeptides; and a method to modulate the interaction of Robo and a Robo ligand. The method is useful for screening for Robo (roundabout) modulators and Robo:Slit complexes are useful for regulating various cell functions, especially of neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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14-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Slit-1 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-347476/29
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   AAY27145 standard; protein; 1529 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 19-21; 34pp; English.
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                                                                                                                                                       662 FNCNCYLAWLGE 673
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                                                                                                                                                                                                                                                                                                                                                                                                                                1 LQAVAVFKQLPEAAALAAANKRVQNLLKKADAALGEVNESLLQQDE-EKALYAAAQGLQP 59
                                                                                                                                                                                                                                                                      SLKTLMLRSNRITCVGNDSFIGLSSVR-LLSLYDNQITTVAPGAFDTLHSLSTLNLLANP
                                                                                                                                                                                                                                                                                                                             KIAAAVAEGNFRTALSE-----LASVKPQVDAFFDGVMVMAEDAAVKQNRLNLLNRLAEQ 114
                                                                                                                                                                                                                                                                                                                                                                                           LEATGIFKKLPQLRKINFSNNKITDIEEGAFEGASGVNEILLTSNRLENVQHKMFKGLE- 602
                                                                                                                                                                                                              MNAVADIALLGE 126
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97US-0065544.
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Matches
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                                                                                                                                                                                                                                                                                                                                     The invention relates to a vertebrate-derived protein containing an amino acid sequence shown in AAY27137 and AAX27139. The vertebrate-derived protein has at least 55 % homology to one of sequences shown in AAY27141-Y27143, and has slit protein-like activity. The vertebrate slit proteins encoding nucleic acid sequences have at least 60% homology to nucleic acid sequences AAX89161-163. The vertebrate-derived proteins can be produced recombinantly by transforming host cells with expression vectors comprising the encoding nucleic acids. The proteins of the invention are for diagnosing and treating cancer of the proteins of the invention are for diagnosing and treating cancer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 58-63; 102pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New vertebrate slit protein - useful for diagnosis and treatment cancers in nerves, muscle and endocrine system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAX89162
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                                                                                                                                                                                                        LQAVAVFKQLPEAAALAAANKRVQNLLKKADAALGEVNESLLQQDE-EKALYAAAQGLQP 59
                                                                                                                  SLKTLMLRSNRITCVGNDSFIGLSSVR-LLSLYDNQITTVAPGAFDTLHSLSTLNLLANP 665
                                                                                                                                                                              LEATGIFKKLPQLRKINFSNNKITDIEEGAFEGASGVNEILLTSNRLENVQHKMFKGLE-
                                                                                                                                              KIAAAVAEGNERTALSE-----LASVKPQVDAFFDGVMVMAEDAAVKQNRLNLLNRLAEQ 114
                                                                                       MNAVADIALLGE 126
                                                                                                                                                                                                                                   al Similarity
33; Conserva
                                                                                                                                                                                                                                                                                                  1529 AA;
                                                                                                                                                                                                                                                                                                                            muscle and/or endocrine system.
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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ALIGNMENTS

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US-08-312-387B-2
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                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                     Matches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver:
CURRENT APPLICATION NOMBER: US/08/312,387B
FILING DATE: July 7, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                  TELEPHONE: 201 487-580
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
LENGTH: 126 amino acid
                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING 1
61 IAAAVAEGNFRTALSELASVKPQVDAFFDGVMVMAEDAAVKQNRLNLLNRLAEQMNAVAD 120
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STATE: New Jersey
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                                                           1 LQAVAVFKQLPEAAALAAANKRVQNLLKKADAALGEVNESLLQQDEEKALYAAAQGLQPK 60
                                     LQAVAVFKQLPEAAALAAANKRVQNLLKKADAALGEVNESLLQQDEEKALYAAAQGLQPK 60
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                                                                                                                 Score 598; DB 1;
Pred. No. 3.7e-57;
); Mismatches 0;
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              US-08-683-458-2
                               RESULT 3
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Sequence 2, Application US/08683458
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                                                                                                                                                                                                                                                                                        Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polocomic
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les 126; Conservative
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)GY: linear
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VERNTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
VENTION: OLICOSACCHARIDES, AND GENES ENCODING THEM
EQUENCES: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     September 26, 1994
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; MOLECULE TYPE: protein US-08-683-458-2
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US-08-878-360-2
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Best Local Similarity
Matches 126; Conserv
                                                                                                                                                                                  Sequence 2, Application US/08878360 Patent No. 5945322
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                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Gotsch
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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PRIOR APPLICATION DATA:
APPLICATION UNMER: 08/312,387
FILING DATE: September 26, 1994
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TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLICOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
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TELEPHONE: 201 487-5800
TELEFAX: 201 343-1884
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                                                                     APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING T
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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STREET: 411
STREET: 411
STREET: 411
TTTY: Hackensack
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                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LQAVAVFKQLPEAAALAAANKRVQNLLKKADAALGEVNESLLQQDEEKALYAAAQGLQPK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LQAVAVFKQLPEAAALAAANKRVQNLLKKADAALGEVNESLLQQDEEKALYAAAQGLQPK 60
                                                                                                                                                                                                                                                                                                 IALLGE 126
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                                    411 Hackensack Avenue
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COMPUTER READABLE FORM:

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US-08-478-140B-2
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; MOLECULE TYPE:
US-08-878-360-2
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                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                  APPLICANT: ROTH, STEPHEN
APPLICANT: BUCZALA, STEPHANIE L.
APPLICANT: BUCZALA, STEPHANIE L.
TITLE OF INVENTION: METHOD OF TRANSFERRING AT LEAST TWO
TITLE OF INVENTION: SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSFERASE,
TITLE OF INVENTION: POLYGLYCOSYLTRANSFERASE AND GENE ENCODING A
TITLE OF INVENTION: POLYGLYCOSYLTRANSFERASE
NUMBER OF SEQUENCES: 8
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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LENGTH: 126 amino acids
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APPLICATION NUMBER:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0
                                                                                                            STREET: 1155 A
CITY: New York
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                                                         COUNTRY: USA
ZIP: 10036-2711
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                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LQAVAVFKQLPEAAALAAANKRVQNLLKKADAALGEVNESLLQQDEEKALYAAAQGLQPK 60
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                                                                                               New York
                                                                                                                               1155 Avenue of the Americas
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Best Local Similarity
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TOPOLOGY: linear
MOLECULE TYPE: protein
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LENGTH: 126 amino acid
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REFERENCE/DOCKET NUMBER: 711
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US,
FILING DATE: 07-JUN-19
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NAME: Laura A. Coruzzi
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SOFTWARE: PatentIn Release #1.0, Version #1.30
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          REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
                                                                                            APPLICATION NUMBER: 08/312,387 FILING DATE: July 7, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                         APPLICATION NUMBER: US/09/33,412
FILING DATE: 15-Jun-1999
CLASSIFICATION: - CUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF OLIGOSACCHARIDES, AND GENES ENCODING THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gotschlich, Emil C.
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                                                      NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                ZIP: 07601
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TELEPHONE: 201 487-5800
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(212) 869-9741/8864
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TELEFAX: 201 343-1684

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ZIP: 10036-2711
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
Tolease #1.0,
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SEQUENCE CHARACTERISTICS:
                                                                   TELEX: 66141 PENNIE (NFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                               SEQUENCE CHARACTERISTICS
                                                                                                                                    NAME: LAURA A. COTUZZÍ
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 710
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Laura A. Coruzzi
                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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Local Similarity 100.0%;
TOPOLOGY:
                  TYPE:
                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                CLASSIFICATION:
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                              ENGTH:
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5. 6379933
                amino acid
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                                  126 amino acids
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VENTION: METHOD OF TRANSFERRING AT LEAST TWO
VENTION: SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSFERASE,
VENTION: POLYGLYCOSYLTRANSFERASE AND GENE ENCODING A
VENTION: POLYGLYCOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                     : (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOHNSON, KARL F. ROTH, STEPHEN
                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.30
linear
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Pred. No. 3.7e-57;
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; MOLECULE TYPE: protein US-09-338-943-2
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Best Local Similarity
Matches 126; Conserv
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Patent No. 5756330
                                                                  Query Match
Best Local
                                                        Matches
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                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                       FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Glumni Edward R
REGISTRATION NUMBER: 38,6
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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553 VADMLEAASALVEVSKEEDFKPSVESLSRAFNLAEKAE-GVATVDSALFENDQEKALAEA 611
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SOFTWARE: FastSEQ
                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                   Local Similarity
                                                                                                                                       TOPOLOGY:
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                            VFKQLPEAAALAAANK----
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for Windows Version
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                          ----RVQNLLKKADAALGEVNESLLQQDEEKALYAA 53
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Pred. No. 3.7e-57;
                                                                    Score 161; DB 1;
Pred. No. 3.5e-09;
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                                                        Mismatches
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; ORGANISM: human
US-09-191-647-2
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US-09-191-647-2
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                               SOFTWARE: Pate
SEQ ID NO 2
LENGTH: 1525
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APPLICANT: Goodman, Corey
APPLICANT: Kid, Thomas
APPLICANT: Kid, Thomas
APPLICANT: Brose, Katja
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/191,647
CURRENT FILING DATE: 1998-11-13
                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09540245A Patent No. 6270984
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Best Local Similarity
                                                                                                                                                                                                                                              APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
                                                                                               PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
RUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/540,245A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/065,544
                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/081,057
EARLIER FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: 60/065,544
EARLIER FILING DATE: 1997-11-14
                       TYPE:
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33;
                                                                                   PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                  Goodman, Corey
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25.0%;
                                                                                                                                          60/081,057
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Pred. No. 0.74;
28; Mismatches
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RESULT 12
US-09-103-664A-2
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                               Sequence 2, Application US/09103664A
Patent No. 6458358
GENERAL INFORMATION:
APPLICANT: University of Kentucky Research Foundation
APPLICANT: Timoney, John
APPLICANT: Artiushin, Sergey
APPLICANT: Artiushin, Sergey
TITLE OF INVENTION: Compounds Encoding the Protective M-Like Protein
TITLE OF INVENTION: and Assays Therefor
FILE REFERENCE: 50229-212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1525
TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,153
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/191,647
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/081,057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1 NUMBER OF SEQ ID NOS:
CURRENT APPLICATION NUMBER: US/09/103,664A
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Kid, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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25.0%;
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; LENGTH: 534
; TYPE: PRT
; ORGANISM: Streptococcus equi
US-09-103-664A-2
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US-08-080-255-7
                                                                    US-08-080-255-7
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NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 534
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Best Local :
Matches
            Query Match
Best Local S
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FILING DATE: 1930617
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:072/P.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Rowley
APPLICANT: Diaz, I
                                                                                                                                                                                           TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: THM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
                                                                                    TOPOLOGY: 1
MOLECULE TYPE:
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ZIP: 772
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Local Similarity 24.7%; Pred. No. 2.8;
es 37; Conservative 21; Mismatches 40; Indels
                                                                                                                     STRANDEDNESS:
                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                            TELEPHONE:
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                Similarity
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 Conservative
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                                                                                    DNA (genomic)
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              12.5%; Score 75; DB 32.6%; Pred. No. 17;
 13;
                                                                                                                                                                                                                                                                   ARCD:072/PAR
 Mismatches
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                                  DB 1;
 25;
                               Length 1400;
 Indels
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 22;
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RESULT 15
PCT-US93-05857-7
; Sequence 7, Application PC/TUS9305857
; GENERAL INFORMATION:
; APPLICANT: Board of Regents
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; Sequence 7, Application
; Patent No. 6121419
; GENERAL INFORMATION:
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Best Local S
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PRIOR APPLICATION NUMBER: US/08/080
APPLICATION NUMBER: US/08/080
FILING DATE: 17 JUNE 1993
ATTORNEY/AGENT INFORMATION:
NAME: PAYKET, DAVIG L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (512) 474-7577 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,71:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 ETSVRGPRIKHVCRRAAVALGRKRAVFPD 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 SIGSMLAQADKLPMTDKRVASLLKKAKAQLCKIEKSKSLKQTDQPK-----AQGQESDSS 281
                                                                                                                                    282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                           Local Similarity
les 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                       5 AVFKQLPEAAALAAANKRVQNLLKKADAALGEV--NESLLQQDEEKALYAAAQGLQ---- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVFKQLPEAAALAAANKRVQNLLKKADAALGEV--NESLLQQDEEKALYAAAQGLQ----
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                                                                                                                                    ETSVRGPRIKHVCRRAAVALGRKRAVFPD 310
                                                                                                                                                                                                      SIGSMLAQADKLPMTDKRVASLLKKAKAQLCKIEKSKSLKQTDQPK---
                                                                                                                                                                   -----PKI-----AAAVAEGNFRTALSE 76
                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (512) 320-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08465713
                                                                                                                                                                                                                                                                           12.5%; Score 75; DB 32.6%; Pred. No. 17; tive 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSLOCATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/465,713
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                                                                                                                                                                                                                                                                            25;
                                                                                                                                                                                                                                                                                                              Length 1400;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05857
FILING DATE: 1930617
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 07/900,689
FILING DATE: 17/06/92
ATTORNEY/AGENT INFORMATION:
NAME: PATKER; DAVIG L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:072/PAR
TELEPHONE: (512) 320-7200
TELEPHONE: (512) 474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1400 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-05857-7
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Search completed: December Job time: 6.69005 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: The University of Texas System
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: GENE REARRANGEMENTS AND TRANSLOCATIONS
NUMBER OF SEQUENCES: 8
                                                                                                                                                  STATE: Texas
COUNTRY: USA
ZIP: 77210
                                                                           282 ETSVRGPRIKHVCRRAAVALGRKRAVFPD 310
                                                                                                                                                                                                                                    y Match 12.5%; Score 75; DB 5; Length 1400; Local Similarity 32.6%; Pred. No. 17; hes 29; Conservative 13; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433 CITY: Houston
                                                                                                                59 -----PKI-----AAAVAEGNFRTALSE 76
                  2, 2002, 12:03:12
                                                                                                                                                                                                                                      25; Indels 22;
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Result
No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                Score
      seq length: 0 seq length: 2000000000
                                                                                                                                                                                                             598
163
                                                                                                                                                                                                                                                                                                                                                     Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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Gapop 10.0 , Gapext 0.5
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598
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   Query
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     126
989
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7271
1289
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      10 US-09-815-242-4897
10 US-09-815-242-5143
10 US-09-815-242-10
10 US-09-815-242-1291
10 US-09-915-242-1291
10 US-09-815-242-1291
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794.504 Million cell updates/sec
Sequence 2, Appli
Sequence 497, Ap
Sequence 5143, Ap
Sequence 259, Appl
Sequence 259, Appl
Sequence 206, Appl
Sequence 12913, A
Sequence 10499, A
Sequence 1703, Ap
Sequence 1703, Ap
Sequence 1856, A
Sequence 1896, A
Sequence 1896, A
Sequence 5814, Ap
Sequence 5815, Ap
Sequence 5815, Ap
Sequence 12967, A
Sequence 12967, A
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US-10-007-267-2
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891	303	874	651	651	577	892	903	891	874	592	592	266	1523	861	234	605	355	2368	2368	1269	1215	1193	1111	635	1043
10	10	10	12	10	10	10	10	10	10	9	9	12	12	10	10	10	10	10	10	10	10	10	10	10	10
-09-272	US-09-925-297-740	US-09-815-242-11809	US-10-007-693-78	-132-	US-09-815-242-13752	US-09-815-242-13843	US-09-905-983-56		5-24	2	US-10-047-593-2	US-10-067-989-3	US-10-052-586-290	US-09-815-242-14088		US-09-841-132-574	US-09-741-669-435	-815-24	-815-24	US-09-815-242-13113	-815-24	-756-071B-	US-09-756-071B-15	US-09-815-242-11209	US-09-946-805-4
5, Ap	Sequence 740, App	1180	Sequence 78, Appl			·ω	Sequence 56, Appl	_	Sequence 11127, A	4,	Sequence 2, Appli	Sequence 3, Appli	Sequence 290, App	14088	Sequence 517, App				5635,		5908	Sequence 13, Appl		Sequence 11209, A	Sequence 4, Appli

ALIGNMENTS

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S-10-007-267-2

S-10-007-267-2

S-Gequence 2, Application US/10007267

Patent No. US20020127682A1

GENERAL INFORMATION:

APPLICANT: GOLSCOLIC, Emil C.

APPLICANT: GLYCOSYLITRANSFERASES FOR BIOSYNTHESIS OF

UNIMER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: ALL Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: DATE: 15 COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATION NUMBER: US/10/007,267

FILING DATE: 15-Un-1999

APPLICATION NUMBER: US/10/007,267

FILING DATE: 15-Un-199

APPLICATION NUMBER: US/10/007,267

FILING DATE: 15-Un-1999

APPLICATION NUMBER: US
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; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: $US-10-007-267-2
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                                                                                                                                   ; NAME/KEY: VARIANT
; LOCATION: (1)...(989)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-815-242-4897
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Best Local Similarity
Matches 126; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                        SEQ ID NO 4897
LENGTH: 989
                                                                                                  Query Match
                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-05-23 PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR
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                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Enterococcus
                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                    ENGTH:
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848 IDAVVSAEQADLSKLFASANILKSRFEDQDFKPSMEALTRVINLAKKGQELLGDTEEGID 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LQAYAYFKQLPEAAALAAANKRYQNLLKKADAALGEVNESLLQQDEEKALYAAAQGLQPK 60
                                                                                    Local Similarity
                                1 LQAVAVFKQLPEAAALAAAN------
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQAVAVFKQLPEAAALAAANKRVQNLLKKADAALGEVNESLLQQDEEKALYAAAQGLQPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carr, Grant J.
Yamamoto, Robert T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zyskind, Judith W.
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                                                                    Conservative
                                                                                    27.3%;
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                                                                    Score 163; DB 10;
Pred. No. 1.1e-08;
9; Mismatches 55;
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US-09-815-242-5143
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SEQ ID NO 5143
LENGTH: 764
TYPE: PRT
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                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                      Query Match
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA 011A
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-12-22
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323 ARKOALAQFA - ANAAAEV 339
                                        103
                                                                              263
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                                                                                                            59 PKIAAAVAEGN-----FRT--ALSELASVKPQVDAFFDGV-MVMAEDAAVKQ 102
                                                                                                                                                                                                                                Local Similarity
les 42; Conserv
                                                                                                                                                                                        2 QAVAVFKQLP---EAAALAAANKRVQNLLKKADAALGEVNESLLQQDEEKALVAAAQGLQ 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SLLQQDEEKALYAAAQGLQPKIAAAVAEGNFRTALSELASVKPQVDAFFDGVMVMAEDA
                          NRLNLLNRLAEQMNAVADI 121
                                                                          VKTAQAQQQANSQISSSQNLISAAFRNQIALAAQASGEAQVTAFNTQVKQIVNEATAFST 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                      QAQQVTQQLGADFNAITTPTATK-VQQRVKAVDASLSQVSTQV-----SGAVASATQAVQ 262
                                                                                                                                                                                                                                                                                                                                                                                                            FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohlsen, Kari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carr, Grant
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                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                    13.0%;
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Pred. No. 3.4;
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                                                                                                                                                                                                                                    53;
                                                                                                                                                                                                                                                                        Length 764;
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US-09-847-539A-10

Sequence 10, Application US/09847539A Patent No. US20020061306A1 GENERAL INFORMATION:

APPLICANT: Bjorck, Lars H

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                                                                                                                                                 ; ORGANISM: Mycobacterium tuberculosis US-09-712-363-259
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                                                           Query Match
Best Local Similarity 25.0
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SEQ ID NO 259
LENGTH: 1289
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SEQ ID NO 10
LENGTH: 271
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Best Local Similarity
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APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS
TITLE OF INVENTION: INVERACTIONS OF PROTEINS
FILE REFERENCE: 07419-032001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rassmussen, Magnus
TITLE OF INVENTION: STREPTOCOCCAL ALPHA ZM BINDING PROTEIN
FILE REFERENCE: 100084 415Us / N.75312B
CURRENT APPLICATION NUMBER: US/09/847,539A
CURRENT FILING DATE: 2001-05-01
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CURRENT FILING DATE: 2000-11-13
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PRIOR FILING DATE: 1999-11-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR
                                                                                                                                                                                      TYPE: PRT
245 IEEAAGVLKHRKRKEKALRKLDTMAANLARLTDLTTELRRQLKPLGRQAEAAQRAAAIQA 30.
                                  10 LPEAAALAAANKRVQNLLKKAD-----AALGEVNESLLQQDEEKALYAAAQGLQPKIAA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 IAAAVAEGNERTALSELASVKPQVDAFFDGVMVMAEDAAVKQNRLNLLNRLAEQMNAVAD 120
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APPLICATION NUMBER: 60/134,092
FILING DATE: 1999-05-14
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                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/
FILING DATE: 1999-11-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1999-02-01
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27.5%;
                                                                        12.6%; Score 75.5; 1
25.0%; Pred. No. 11;
Live 21; Mismatches
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Pred. No. 1.
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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Best Local Similarity
Matches 30; Conserv
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12913, Application US/09815242 Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Geiger, Benjamin
APPLICANT: Ben-Ze'ev, Avri
APPLICANT: Sadot, Einat
TITLE OF INVENTION: METHODS AND THERAPEUTIC COMPOSITIONS FOR TREATING CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 01/23326
CURRENT APPLICATION NUMBER: US/09/905,983
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 60
                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITER.011A
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 ASQAFLRHPDVAATRANRDYVFKQVQEATAGISSAAQATSPTDEAKGHTGIGELAAALNE 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305
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                                                                                                                                                                                                                                                                                         Xu, H. Howard
                                                                                                                                                                                                                                                                                                      Carr, Grant J.
Yamamoto, Robert T.
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Pred. No.
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7.7;
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PRIOR FILLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILLING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 12913
LENGTH: 2186
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12913
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 08/833,457
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 370
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 206
LENGTH: 400
TYPE: PRT
ORGANISM: Helicobacter pylori
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RESULT 9
US-09-815-242-10499
; Sequence 10499, Application US/09815242
; Patent No. US20020061569A1
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US-09-881-752A-206
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020115078Ale1 Helicobacter Polypeptides in the
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/041002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/881,752A
CURRENT FILING DATE: 2001-06-15
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                                                                                                                                                 72 TALSELASVKPQVDAFFDGVMVMAEDAAVKQNRLNLLNRLAEQMNAV 118
                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                       QNLASSNDVVLQVAFENLHQSTLSKMSQLSQEEKELNTQALKVKNSIQKISSIIDEQKTR 187
                                                                                                                 EV--TLKSLKTEQDKL---ILSMQKDYAIYNQRLTLLEKERQNLNAL 229
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Tomb, Jean-Francois
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25.8%;
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/2191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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APPLICANT: Haselbeck, Robert
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                                                                                                                                                                                                                                                                                                                 Sequence 5703, Application Patent No. US20020061569A1
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
FILE TEREFERENCE: ELITRA.011A
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                    APPLICANT:
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TYPE: PRT
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nes 31; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 KQLPEAAALAAANKRVQNLLKKADA-------ALGEVNESLLQQDEEKALYA 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --DGVMVMAEDAAVKQ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAKEMPEISEDGKRYTIKLREDGKWSNGDAVTANDFVFAWRKLANPKNQANYFFLLEGT 146
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Yamamoto, Robert T.
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22.8%; Pred. No. 5
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; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-815-242-5703
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 5703
LENGTH: 2025
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12611, Application Patent No. US20020061569A1
                                                                                          PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
SOFTWARE: FastSEQ for Windows Version SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Identification of Essential Genes
                                     NUMBER OF SEQ ID NOS:
                                                    PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/269,308
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APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
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                                                                           APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                               APPLICATION NUMBER: 60/242,578
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Zyskind, Judith W.
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US-09-815-242-11856
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
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PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                               LENGTH: 393
TYPE: PRT
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108 -LNRLAEQMNAVADIALLG 125
                                                                                                           154 DYHMGITAENLAEKYGLTREEQDAFAAAS--QQKAIAAIEGGRFRDEITPIQVPQRKGEP 211
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                                      LGFDTDEQPRAGTTVEALAKLKPAFRKDGSVTAGNASSLNDGAAAVLLMSAAKAKALGLP
                                                                      ------TALSELASVKP------QVDAFFDGVMVMAEDAAVKQNRLNL- 107
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                                                                                                                                                                                    Conservative
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Pred. No.
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Pred. No. 5
                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                    43; Indels
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US-09-815-242-5834

Patent No. Sequence 5834,

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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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SOFTWARE: FastSEQ for Windows Version
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/2
PRIOR FILING DATE: 2000-05-26
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APPLICANT:
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                     APPLICANT: Xu, H. I
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TITLE OF INVENTION:
                                                       APPLICANT:
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DR FILING DATE: 2000-10-23
DR APPLICATION NUMBER: 60/253,625
DR FILING DATE: 2000-11-27
DR APPLICATION NUMBER: 60/257,931
DR APPLICATION NUMBER: 60/257,931
DR FILING DATE: 2000-12-22
DR FILING DATE: 2000-12-22
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Trawick, John D.
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                                                                                                                  Zyskind, Judith W. Wall, Daniel
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                                                                                                                                                        Ohlsen, Kari L.
                                                                           Carr, Grant J.
                                                                                              Trawick, John D.
                                                         Yamamoto, Robert T
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0020061569A1
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                                         H. Howard
                     [dentification of Essential Genes
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26.0%;
   Prokaryotes
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Pred. No. 64;
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SOFTWARE: FastSEQ for
SEQ ID NO 12996
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                         Matches
                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: STREPTOCOCCAL ALPHA ZM BINDING FILE REFERENCE: 100084.415US / N.75312B CURRENT APPLICATION NUMBER: US/09/847,539A CURRENT FILING DATE: 2001-05-01 NUMBER OF SEQ ID NOS: 30
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                                           Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bjorck, Lars H
APPLICANT: Rassmussen, Ma
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TYPE: PRT
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                                   61 IAAAVAEGNFRTALSELASVKPQVDAF--FDGVMVMAEDAAVKQNRLNLLNRLAEQMNAV 118
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 EAAVVQSDN--AASDALEALADQTDALQSEEAAVVKADNAA----SDTLEALADQTDAL
                                                                         PEKLALRNEERAIDELKKQAIEDKEATTAIEAASSDALEALADQ------ADALQSE 95
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27.5%; Pred. No.
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Search completed: December 2, 2002, 12:15:58 Job time : $5.52541 \ \text{secs}$

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Result
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         GB1027
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82.5	82.5	82.5	83	83.5	84	84.5	84.5	86	86.5	86.5	91	92.5	103.5	119	121
13.8	13.8	13.8	13.9	14.0	14.0	14.1	14.1	14.4	14.5	14.5	15.2	15.5	17.3	19.9	20.2
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paramyosin - nemat	160K golgi antigen	hypothetical prote	arginyl-tRNA synth	Htr5 transducer [i	transducer protein	Htrl3 transducer [probable decarboxy	secreted leucine-r	hypothetical prote	halobacterial tran	RTX toxin transpor	glycyl-tRNA synthe	glycyl-tRNA synthe	probable aminoacyl	glycine-tRNA ligas

ALIGNMENTS

RESULT 2 G81970	Qy 1 LQAVAVFKOLPEAAALAAANKRVQNLLKKADAALGEVNESLLQQDEEKALYAAAQGLQPK 60	A;Status: preliminary A;Status: preliminary A;Status: preliminary A;Molecule type: DNA A;Residues: 1-687 crefrences: GB:AE002541; GB:AE002098; NID:g7227175; PIDN:AAF42259.1; PID:g722 A;Cross-references: GB:AE002541; GB:AE002098; NID:g7227175; PIDN:AAF42259.1; PID:g722 A;Genetics: A	RESULT 1 B81027 Glycyl-trnA synthetase, beta chain NMB1930 [imported] - Neisseria meningitidis (strai glycyl-trnA synthetase, beta chain NMB1930 [imported] - Neisseria meningitidis (strai glycyl-trnA synthetase, beta chain NMB1930 [imported] - Neisseria meningitidis (strai glycyl-trnA synthetase, beta change 19-Jan-2001 C; Paccless: Neisseria meningitidis C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C; Acclession: E81027 R; Tettelin, H.; Sanders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. Ti. H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000 A; Anthors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A; Reference number: A81000; MUID: 20175755; PMID: 10710307 A; Accession: E81027

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RESULT 3
$778812
glycine-tRNA ligase (EC 6.1.1.14) - Neisseria meningitidis (fragment)
N;Alternate names: glycyl tRNA synthetase
C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 03-Jun-2002
C;Accession: $70812
R;Jennings, M.P.; Hood, D.W.; Peak, I.R.A.; Virji, M.; Moxon, E.R.
Mol. Microbiol. 18, 729-740, 1995
A;Title: Molecular analysis of a locus for the biosynthesis and phase-varial A;Reference number: $70812; MUID:96414473; PMID:8817494
A;Accession: $70812
A;Status: preliminary; nucleic acid sequence not shown; translation not shown.
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-687 <PAR>
A;Cross references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83815.1; PID:g737926
A;Cross references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83815.1; PID:g737926
         glycyl-tRNA synthetase, beta chain VC0020 [Imported] - VLULIO CILLELLO VCC. C;Species: Vibrio cholerae C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Date: 18-Aug-2000 #text_change 02-Feb-2001 C;Date: 18-Aug-2000 #text_change 02-Feb-2001 T;Date: 18-Aug-2001 T;Date: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U25839; NID:g973183; A;Note: the nucleotide sequence was submitted C;Genetics:
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C;Superfamily: glycine-tRNA ligase
C;Keywords: ligase
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C;Superfamily: glycine-tRNA ligase
C;Keywords: ligase
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I.; Sellers,
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glycine-tRNA ligase (EC 6.1.1.14) beta chain - Haemophilus influenzae (stra N.Alternate names: glycyl-tRNA synthetase beta chain C:Species: Haemophilus influenzae (stra C:Species: Haemophilus influenzae (c.pate: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 03-Jun-2002 (c.pate: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 03-Jun-2002 (c.paccession: B64103
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A;Molecule type: DNA
A;Residues: 1-688 <HEI>
A;Cross-references: GB:AE004094; GB:AE003852; NID:g9654407; PIDN:AAF93198.1;
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
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C; Superfamily: glycine-tRNA ligase beta
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A;Accession: F82373
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A; Residues: 1-688 <TIGR>
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52.8%; Pred. No. 7.4e-17;
Live 23; Mismatches 35
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Pred. No. 4.5e-15;
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#text_change

31-Dec-2000

Pseudomonas

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glycine tRNA synthetase beta subunit [imported] - Escherichia coli (strain c;Species: Escherichia coli (strain C;Species: Escherichia coli (c;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C;Accession: B91184
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R; Stover, C.K.; Pham, X.Q.; Erwin,
adman, S.; Yuan, Y.; Brody, L.L.; (
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Nature 406, 959-964, 2000
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C; Superfamily:
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A;Residues: 1-689 <HAY>
A;Residues: 1-689 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB37865.1; PID:913363916; GSPDB:GN00154
A;Experimental source: strain o157:H7, substrain RIMD 0509952
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DNA Res. 8, 11-22, 2001
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C;Superfamily: glyci
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A;Molecule type: DNA
A;Residues: 1-684 <STO>
 Дb
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status:
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                                                                                                                                                                                                                   Matches
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                                                                                                                                                                         1 LQAVAVFKQLPEAAALAAANKRVQNLLKKADAALGE-VNESLLQQDEEKALYAAAQGLQP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LQAVAVFKQLPEAAALAAANKRVQNLLKKA-DAALGEVNESLLQQDEEKALYAAAQGLQP 59 : | | | | | | | | | | | | : | | : | | : | | : |
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DISLL
                                   DIALL 124
                                                                                        KIAAAVAEGNFRTALSELASVKPQVDAFFDGVMVMAEDAAVKQNRLNLLNRLAEQMNAVA 119
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                                                                                                                                         MKAVSHFRTLEAAAALAAANKRVSNILAKSDEVLSDRVNASTLKEPEEIKLAMQVVVVLRD 623
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                                                                   KLEPYFAEGRYQDALVELAELREPVDAFFDKVMVMVDDKELRINRLTMLEKLRELFLRVA
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Yasunaga, T.; Kuhara, S.;
                                                                                                                                                                                                                                                                                       glycine-tRNA ligase beta chain
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 889
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                                                                                                                                                                                                                                42.2%; Score 252.5;
48.0%; Pred. No. 2.3
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Pred. No. le
                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kurokawa, K.; Ishii, K.; Yokoyama,
Shiba, T.; Hattori, M.; Shinagawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .5; DB
le-13;
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A.; Larbig,
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K.; Lim,
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RESULT

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R:Keng, T.; Webster, T.A.; Sauer, R.T.; Schimmel, P.R.
J. Biol. Chem. 257, 12503-12508, 1982
A:Title: Gene for Escherichia coli glycyl-tRNA synthetase
A:Reference number: I41241; MUID:83030764; PMID:6290471
A:Accession: I41242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glycine-tRNA ligase (EC 6.1.1.14) beta chain - Esch N;Alternate names: glycyl-tRNA synthetase beta chai C;Species: Escherichia coli C;Date: 28-Aug-1985 #sequence_revision 17-May-1996 C;Accession: $47780; 141242; A01189; A65155 R;Plunkett, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1,'Q','3-90,'P',92-153,'AAA',157-210,'DG',213-341,'D',343-360,'V',362-689
A;Residues: 1,'Q','3-90,'P',92-153,'AAA',157-210,'DG',213-341,'D',343-360,'V',362-689
A;Ross references: GB:J01622; NID:g146221; PIDN:AAA23915.1; PID:g146223
A;Note: the authors translated the codons GAC and GTC for residues 342 and 361 as Leu
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A; Rose, D.J.; Mau, B;Shao, Y.
Science 277, 1453-1462, 1997
                                                                                                                                                                                   A;Cross-references: GB:J01623; NID:g146224; PIDN:AAA23917.1; PID:g146226 R;Webster, T.A.; Gibson, B.W.; Keng, T.; Biemann, K.; Schimmel, P. J. Biol. Chem. 258, 10637-10641, 1983 J. Biol. Chem. 258, 10637-10641, 1983 A;Title: Primary structures of both subunits of Escherichia coli glycyl-trNA A;Reference number: A92392; MUID:83290996; PMID:6309809 A;Accession: A01189
                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-20 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data
A; Reference number: S47666
A; Accession: S47780
A; Molecule type: DNA
A; Residues: 1-689 <PLU>
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C;Superfamily: glycine-tRNA ligase beta chain
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-689 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Genome sequence of enterohemorrhagic Escherichia A; Reference number: A85480; MUID:21074935; PMID:11206551
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complete genome
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sequence of
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Pred. No. 2.3
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Escherichia coli K-12
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A;Gene: glyS; glyS(b)
A;Map position: 80 min
C;Complex: tetramer of two alpha and two beta chains
C;Superfamily: glycine-tRNA ligase beta chain
C;Keywords: aminoacyl-tRNA synthetase; ligase; prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: AH0494
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
Nature 413, 523-527, 2001
                       RESULT
AI0980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: glyS
C;Superfamily: glycine-tRNA ligase beta chain
C;Keywords: ligase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glycine-trNA ligase (EC 6.1.1.14) [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 03-Jun-2002
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glycine-tRNA ligase (EC 6.1.1.14)
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                                                                                                                     DISLL 688
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                                                                                                                                                                                                                                                                                                                                                                                         40.4%; Score 241.5; DB 2
46.4%; Pred. No. 1.8e-12;
ative 23; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.6%; Score 248.5; DB 1
47.2%; Pred. No. 4.9e-13;
tive 21; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN:CAC93524.1;
       Salmonella
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A; Contents: annotation C; Genetics:

A; Gene: XF1959 C; Superfamily:

glycine-tRNA ligase beta chain

M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, A;Reference number: A59328

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A;Cross-reterences observed A;Cross-reterences observed A;Cross-reterences observed A;Cross-reterences observed A;Experimental source: strain 9aSc R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fra; D.J.; Junqueira, V.C.A.; Ferro, J.A.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La Chado, M.A.; Madeira, M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodriques, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, F.R.; da Silva, A.M.; Vertore, A.L.
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella en
A;Reference number: AB0502; PMID:11677608
A;Accession: AI0980
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; V
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: A82617
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C;Superfamily: glycine-tRNA ligase beta chain
C;Keywords: ligase
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A; Residues: 1-722 <SIM>
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A; Residues: 1-689 < PAR>
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Pred. No. 1.8e-11;
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, L.; White,
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Ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58
A;Reference number: AB2577; PMID:11743193
A;Accession: AF2655
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-717 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL41660.1; PID:g17739002; GSPDB:GN00186
                                                                                                                                                                                                                                                                                                                glycyl-tRNA synthetase, beta chain glyS [imported] - Agrobacterium tumefaciens (strain of Species: Agrobacterium tumefaciens C. Species: Agrobacterium tumefaciens C. Species: Agrobacterium tumefaciens C. Species: Agrobacterium tumefaciens C. Accession: AF2655 C. Accession: AF2655 R. Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, P.; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
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B97437

Glycyl-tRNA synthetase, beta chain nmb1930 [imported] - Agrobacterium tumefaciens (straiglycyl-tRNA synthetase, beta chain nmb1930 [imported] - Agrobacterium tumefaciens (straiglycyl-tRNA synthetase, beta chain nmb1930 [imported] - Agrobacterium tumefaciens (straiglyspecies: Agrobacterium tumefaciens) (straiglyspecies: Agrobacterium tumefaciens (straigly
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AF2655
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                                                                                                                                                                                                                                                    A; Authors: Yoo, H.; Tao, ster, E.W.
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A;Molecule type: DNA
A;Residues: 1-717 <KUN>
A;Cross-references: GB:AE007869; PIDN:AAK86451.1; PID:g15155593; GSPDB:GN00169
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A;Map position: ci
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                                                                                                                                                                                                                                                                                  Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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41.0%; Pred. No. 7.7
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Pred. No. 4.4e-08;
0; Mismatches 54;
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Search completed: December Job time: 6.59198 secs

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771 KVADFS 776

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glycine-tRNA ligase (EC 6.1.1.14) [imported] - DALULLIAN GRAND GRA
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C;Superfamily: glycine-tRNA ligase
C;Keywords: ligase
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A; Map position:
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A; Residues: 1-780 < KUR>
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       AVADIA 122
                                                                                                             LQAVAVFKQLPEAAALAAANKRVQNLL----KKADAALGEVNESLLQQDEEKALYAAAQG 56
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35.7%;
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Pred. No.
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Glycyl-tRNA synthetase
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16-OCT-2001
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Bacteria; Proteobacteria;
CGBI_TaxID=666;
                                                                                                                                                                                                                                                         Complete proteome
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PROSITE; PS50861; AA_TRNA_LIGASE_II_GLYAB;
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Pfam; PF02092; tRNA_synt_2f; 1.
                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE004094; AAF93198.1; TIGR; VC0020; -.
                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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-!- CATALYTIC ACTIVITY: ATP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
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STRAIN=El Tor N16961 / Serotype 01;
MEDLINE=20406833; PubMed=10953301;
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                                                                                                                                                                                                                                                                           Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 682
                            120
                                                            622
                                                                                                                       562
                                                                                         60
                                                                                                                                     SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   + glycyl-trna(Gly).
SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS
               DIALL 124
DISLL 686
                                                          ALEPAFATGNYQEALSKLAGLRAPVDAFFDNYMYMADDEALKKNRLTLLNKLRNLFLQIA
                                                                                  KIAAAVAEGNERTALSELASVKPQVDAFFDGVMVMAEDAAVKQNRLNLLNRLAEQMNAVA 119
                                                                                                                       VKAVSHFRALEEAEALAAANKRVGNILAKYDGELGEEIDLALLQEDAEKALAEAVEIMAE 621
                                                                                                                                                                                  1 Similarity
66; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 40,
(Rel. 40,
(Rel. 40,
                                                                                                                                                                                                                                              889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GlyRS).
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                              ΑΑ,
                                                                                                                                                                                                                                              75924 MW;
                                                                                                                                                                                                  49.2%; 52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
e beta chain (EC 6.1.1.14) (Glycine--tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma subdivision; Vibrionaceae; Vibrio
                                                                                                                                                                                   23;
                                                                                                                                                                                                   Score 294.5;
Pred. No. 2.
                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glycine + tRNA(Gly) = AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                              9B6A9A21715D2B39
                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                   .8e-17;
                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                Length
                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diphosphate
                                                                                                                                                                                   1;
                                                                                                                                                                                   Gaps
                                                               681
                                                                                                                                                        59
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RESULT 4
SYGB_HAEIN
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SYGB_HAEAE
OX OCC
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                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                     P43822;
01-NOV-1995 (Rel. 32, Cr
01-NOV-1995 (Rel. 32, La
15-JUN-2002 (Rel. 41, La
Glycyl-tRNA Synthetase b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998
15-JUL-1998
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002311; tRNA_synt_2f.
Pfam; PF02092; tRNA_synt_2f; 1.
PROSITE; PS50861; AA_TRNA_LIGASE_II_GLYAB; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase;
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycyl-tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         030836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYGB_HAEAE
                                               beta chain) (G. GLYS OR HI0924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                + glycyl-trna(Gly).
-!- SUBUNIT: TETRAMER OF TWO ALPHA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=F3031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus
                     Haemophilus influenzae.
Bacteria; Proteobacteria;
                                                                                                                                     SYGB_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE

    -!- SUBCELLULAR LOCATION: Cytoplasmic.
    -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=725;
 NCBI_TaxID=727;
           Haemophilus
                                                                                                                                                                                                 281
                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                               221
                                                                                                                                                                                                                                                                                                161
                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                       1 LQAVAVFKQLPEAAALAAANKRVQNLLKKADAALGEVNESLLQQDEEKALYAAAQGLQPK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY).
                                                                                                                                                                                                                                                                                               VRAVSHFRTLDSAEALAAANKRVSNILAKADAAIGEINLTVCVEQAEKALAEAVLALRTE 220
                                                                                                                                                                                                                          IALL
                                                                                                                                                                                                                                              VQPLIEQGDYTTVLDKLANLRAPVDSFFDNVMVNAEDPALRQNRLAILNTLQGLFLQVAD
                                                                                                                                                                                                                                                            IAAAVAEGNFRTALSELASVKPQVDAFFDGYMYMAEDAAVKQNRLNLLNRLAEQMNAVAD 120
                                                                                                                                                                                                 ISVL
                                                                                                                                                                                                                                                                                                                                                 59;
                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 (Rel. 36, Created)
98 (Rel. 36, Last sequence upd
91 (Rel. 40, Last annotation u
91 (Rel. 40, Last annotation u
91) (GlyRS) (Fragment).
                                                                                                                                                                                                   284
                                                                                                                                                                                                                          124
                                                                                                                                                                                                                                                                                                                                                                                                  285 AA;
                                                                    (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aegyptius.
                                     influenzae
                                                            (GlyRS).
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                  30957 MW;
                                                                                                                                                                                                                                                                                                                                                          46.5%;
47.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gamma
                        gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence update)
                                                                                                                                                                                                                                                                                                                                                 27;
                                                                                                                                                                                                                                                                                                                                                            Score 278; DB 1;
Pred. No. 2.5e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                  034C4EE695DBB138 CRC64;
                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subdivision;
                          subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
6.1.1.14) (Glycine--tRNA ligase
                                                                          update)
6.1.1.14)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BETA CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pasteurellaceae;
                          Pasteurellaceae,
                                                                                                                                                                                                                                                                                                                                                                         Length 285;
                                                                          (Glycine--tRNA ligase
                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                          ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a collaboration -
                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outstation
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RESULT
SYGB_EC
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                                                                                                                                                                                                                                                   망
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 59
                                               SYGB_ECOLI STANDARD; PRT; 688 AA.

P00961;

1 21-UUL-1986 (Rel. 01, Created)

1 16-EB-1995 (Rel. 31, Last sequence update)

1 16-CCT-2001 (Rel. 40, Last annotation update)

2 Glycyl-trna synthetase beta chain (EC 6.1.1.1

B beta chain) (GlyRS).

B GIYS OR GLYS (B) OR B3559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M. McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Keiley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C. Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TOTAL ATCC 51907;
TOTAL PubMed=75428
                                                                                                                                                                                     ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGR00211; glyS; 1.

PROSITE; PS50861; AA_TRNA_LIGASE_II_GLYAB; 1.

Aminoacyl-trNA_synthetase; Protein biosynthesis; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U32774; AAC22584.1; -.
TIGR; HI0924; -.
InterPro; IPR002311; tRNA_synt_2f.
Pfam; PF02092; tRNA_synt_2f; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 269:496-512(1995).
-i- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Rd / KW20 / ATCC 5170/,
MEDLINE=95350630; PubMed=7542800;
              Escherichia
                          Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
                                            Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01045; TRNASYNTHGB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                              564
                                                                                                                                                                                                                                                   684
                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                              624
                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                      1 LQAVAVFKQLPEAAALAAANKRVQNLLKKADAALGEVNESLLQQDEEKALYAAAQGLQPK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    + glycyl-tRNA(Gly).
SUBUNIT: TETRAMER OF TWO ALPHA AND
                                                                                                                                                                                                                                                 ISVL
                                                                                                                                                                                                                                                                                                            VQPLIAQGDYTTVLDKLANLRAPVDSFFDNVMVNAEDPALRQNRLAILNTLQGLFLQVAD
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                                                                                                                                                                                                                                                                               IALL
                                                                                                                                                                                                                                                                                                                                                                         VRAVSHFRTLDSAEALAAANKRVSNILAKAGAAIGEINLTACVEPAEKALAEAVLALRTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                           IAAAVAEGNERTALSELASVKPQVDAFFDGVMVMAEDAAVKQNRLNLLNRLAEQMNAVAD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                            59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteome.
                                                                                                                                                                                                                                                   687
                                                                                                                                                                                                                                                                               124
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                                            co1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75612 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.7%;
47.6%;
                           gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 273; DB 1;
Pred. No. 1.7e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67F9ACEF00A94184
                           subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                     update)
6.1.1.14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TWO BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clayton R.A., Kirkness E.F.,
Dougherty B.A., Merrick J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                      (Glycine--tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a collaboration - MBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                          623
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Matches
                                                                        COMPLETE
INIT_MET
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-19 FROM N.A. MEDILINE-83030764; PubMed=6290471; MEDILINE-83030764; PubMed=6290471; Keng T., Webster T.A., Sauer R.T., Schimmel P.; "Gene for Escherichia coli glycyl-tRNA synthetase has tandem subunit coding regions in the same reading frame."; J. Biol. Chem. 257:12503-12508(1982).
                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Comparing the predicted and observed properties of in the genome of Escherichia coli K-12."; Electrophoresis 18:1259-1313(1997).
-!- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Analysis of the Escherichia coli genome. V. DNA sequence of the region from 76.0 to 81.5 minutes.";
Nucleic Acids Res. 22:2576-2586(1994).
                                                                                                                                                                    PRINTS; FRALLOW, TIGRO0211; glyS; 1.
TIGREAMS; TIGRO0211; glyS; 1.
PROSITE; PS50861; AA TRNA_LIGASE_II_GLYAB; 1.
PROSITE; PS50861; AA TRNA_LIGASE_II_GLYAB; 1.
                                                                                                                                                                                                                                                  ECOGENE; EG10410; glyS.
ECOGENE; EG10410; glyS.
InterPro; IPR002311; tRNA_synt_2f.
InterPro; IPR002311; tRNA_synt_2f; 1.
                                                                                                                                                                                                                                                                                                                          EMBL; J01622; AAA23915.1; -. EMBL; U00039; AAB18536.1; -. EMBL; AE000433; AAC76583.1; -. EMBL; J01623; AAA23917.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE: .... MG1655;
STRAIN=KIZ / MG1655;
MEDLINE=94316500; PubMed=8041620;
MEDLINE=94316500; PubMed=8041620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthetase
                                                          SEQUENCE
                                                                                                                                                                                                                                                                                             PIR; A01189; SYECGB.
ECO2DBASE; E077.5; 6TH EDITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K12 / EMG2;
MEDLINE=97443975; PubMed=9298646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Webster T.A., Gibson B.W., Keng T., Biemann K., Schimmel P. ^{\text{m}}Primary structures of both subunits of Escherichia coli gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-83290996; PubMed-6309809;
Webster T.A., Gibson B.W., Keng T., Biemann K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Link A.J., Robison K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glycyl-tRNA(Gly).
                                                                                                                                                                                                                                       PR01045; TRNASYNTHGB.
                Similarity
                                                          688 AA;
                                                                      0
190
153
210
341
360
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258:10637-10641(1983)
                                                                        90
155
211
341
360
                41.6%;
                                                          76681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Church G.M.;
                                                          ₩.
 21;
                                                                   S -> Q (IN REF. 1).
A -> P (IN REF. 1).
DVH -> AAA (IN REF. 1).
ER -> DG (IN REF. 1).
L -> D (IN REF. 1).
L -> V (IN REF. 1).
                Pred. No.
                             Score 248.5;
                                                          DDA27FF5DBC4BE3B
 Mismatches
               1.9e-13;
                             DB 1;
 44;
                                                          CRC64;
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 Indels
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1 LQAVAVFKQLPEAAALAAANKRVQNLLKKADAALGE-VNESLLQQDEEKALYAAAQGLQP 59

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RESULT
SYGB_CO
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P45651;
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MEDLINE=94350801; PubMed=8071197;
Suhan M., Chen S.Y., Thompson H.A., Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coxiella group;
NCBI_TaxID=777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycyl-tRNA
                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                            This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished observations (AUG-1995).
-!- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bairoch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning and characterization of an autonomous from Coxiella burnetii.";
J. Bacteriol. 176:5233-5243(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coxiella burnetii.
Bacteria; Proteobacteria;
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                                                                                                                                                                                                            EMBL; U10529; AAA550313.1; ALT_FRAME.
InterPro; IPR002106; AACTRNA_11gaseII.
InterPro; IPR002311; tRNA_synt_2f.
Pfam; PF02092; tRNA_synt_2f; 1.
                                                                                                                                                                                                                                                                                                                                                              between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             683
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                                                                                                                                                                                 Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase;
                                                                                                                                                                                                   PROSITE;
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SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS.

SUBCELLULAR LOCATION: Cytoplasmic.

SUBCELLULAR LOCATION: Cytoplasmic.

SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.

CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THREE FRAMESHIFTS WERE

INTRODUCED TO MAXIMIZE THE SIMILARITY WITH ORTHOLOGS IN OTHER
                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISLL
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                                                                LQAVAVFKQLPEAAALAAANKRVQNLLKKADAALGEVNESLLQQDEEKALYAAAQGLQPK 60
          IAAAVAEGNERTALSELASVKPQVDAFEDGVMVMAEDAAVKQNRLNLLNRLAEQMNAVAD 120
                                       IKAVQHFQTLPEADALAAANKRVSNILKKQAAELKSIDHSLFDSDAEHLLADQLKERAEL 219
                                                                                                             Similarity
                                                                                                                                                                                                   PS50861; AA_TRNA_LIGASE_II_GLYAB;
                                                                                                                                                                                                                                                                                                                               non-profit institutions as long as its content
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5 (Rel. 32, Last sequence upd
12 (Rel. 41, Last annotation u
1A synthetase beta chain (EC 6
1) (GlyRS) (Fragment).
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                                                                                                Score 238; DB Pred. No. 5.3e 21; Mismatches
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6.1:1.14) (Glycine--tRNA ligase
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SYGB_XYLFA RESULT 8

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Best Local :
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Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-!- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP + diphosphate + glycyl-tRNA(Gly).
-!- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO RETA CUATTO ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glycyl-tRNA synthetase beta chain (EC 6.1.1.14) (Glycine--tRNA ligase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21145866; PubMed=11248100; May B.J., Zhang Q., Li L.L., Paustian M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pasteurella multocida
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Pfam; PF02092; tRNA_synt_2f; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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684
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DISLL
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                                                                                                                                                                                                            VRAVSHFRALEAAEALAAANKRVSNILAKVEGELPANIDTTLCAEAAEKVLAEQVIALQA 623
                                                                                                    ELAPLFAKGEYQVALDRLAALREPVDTFFDNVMVNAENPQLRQNRLAILNNLRNLFLQVA
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PS50861; AA_TRNA_LIGASE_II_GLYAB;
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RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Fullan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Kitajima J.P.,
RA HO P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA HO P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Lalgret F., Lambais M.R., Leite L.C.C.,
Lemos E.G.M., Lemos M.V. F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matrino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Manni A., Jr., Nobrega F.G., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T., O., Netto L.E.S.,
RA Moon D.H., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA Quaggio R.B., Roberto P.G., Santelli R.V., Sawasaki H.E.,
RA de Solva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva A.C.R., da Silva H.M. Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Cago M.A., Zatz M., Meidanis J., Setubal J.C.;
"The genome sequence of the plant pathogen Xylella fastidiosa.";
R. Lature 406:151-159(2000)
    Matches
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Q9PC26;
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                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glycyl-tRNA synthetase beta chain (EC 6.1.1.14) (Glycine--tRNA ligase
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                                                                                                                                        PRINTS; PR01045; TRNASYNTHGB.
TIGREAMS; TIGR00211; glyS; 1.
PROSITE; PS50861; AA_TRNA_LIGASE_II_GLYAB;
                                                                                                                                                                PRINTS; PR01045;
TIGRFAMS; TIGR002
                                                                                                                                                                                                      InterPro; IPR002311; tRNA_synt_2f.
Pfam; PF02092; tRNA_synt_2f; 1.
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                                                                                                                       Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase;
                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 + glycyl-trna(gly).
SUBUNIT: TETRAMER OF TWO ALPHA AND
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                                                                                   80149 MW;
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                       Score 210.5;
Pred. No. 2.
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G1ycy1-trna;
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Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
Haft D.H., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
Evidence for lateral gene transfer between Archaea and Bacteria fro
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peta chain) (GlyRS).
GLYS OR TM0217.
                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Thermotogae; The Thermotogaceae; Thermotoga
                                                                                                                                                                        TIGRFAMS; TIGR00211; glyS; 1
PROSITE; PS50861; AA_TRNA_LIGASE_II_GLYAB;
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546 EALQEISEKPEFQDLFVGFERVHNITKNHDST--KFDGALFEKEEEKKLMNKFYEVKEKV 603
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                              2 QAVAVFKQLPEAAALAAANKRVQNLLKKADAALGEVNESLLQQDEEKALYAAAQGLQPKI 61
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SIMILARITY: BELONGS TO
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672 AA;
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(Rel. 40, Last sequence update)
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synthetase beta chain (EC 6.1.1.14)
                                                                 Conservative
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                                                                              Score 151;
Pred. No. 2.
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Rickettsia prowazekii.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glycyl-trna synthetase beta chain (EC 6.1.1.14) (Glycine--trna ligase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99039499; PubMed=9823893;
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rickettsiaceae; Rickettsieae; NCBI_TaxID=782;
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InterPro; IPR002311; tRNA_synt_2f.
Pfam; PF02092; tRNA_synt_2f; 1.
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PROSITE; PS50861; AA_TRNA_LIGASE_II_GLYAB; 1.
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SUBUNIT: TETRAMER OF TWO ALPHA AND
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CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
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                                                        ELASVKPQVDAFFDGVMVMAEDAAVKQNRLNLLNRLAEQMNAVADIALL
                                                                                                                                                                             LAAANKRVQNLLKKADAALGEVNESLLQQDEEKALYAAAQGLQPKIAAAVAEGNFRTALS 75
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LLSSLLKPITSFFDNVLVNDSDPKIAQNRLSLLQNTCEVFDKVAKFCRL
                                                                                                                    LLNAYKRVSNIMGN-QKITGLVDASLFSTQYEKELFEVIQKISQQIIVIIANKDYQKALN
                                                                                                                                                                                                                                                                         Similarity
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RESULT 11

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RA Kunst F. Ogasawara N. Moszer I. Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braum M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Chim S.Y., Glaser P., Goffeau A., Galizzi A., Galleron N.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Seadie Y.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Rakeuchi M., Tanakoshi A., Tanaka T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Tarahashi H., Takemaru K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
The complete genome sequence of the Gram-positive bacterium Bacillus
The complete genome sequence of the Gram-positive bacterium Bacillus
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01-OCT-1996
15-JUN-2002
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MEDLINE=97124195; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mizuno M., Masuda S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes;
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                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                        -1- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS.
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98044033; PubMed=9384377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microbiology 142:3103-3111(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                           Nature 390:249-256(1997).
                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP + diphosphate
                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
    D84432;
Z99116;
                                                                                                                                                                                                                                                                                    glycyl-tRNA(Gly)
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(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
synthetase beta chain (EC 6.1.1.14) (Glycine--tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GlyRS).
  BAA12485.1;
CAB14455.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takemaru K.-I., Hosono S.,
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RESULT 12
SYGB_AQUAR
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
619CY1-tRNA synthetase beta chain (EC 6.1.1.14) (Glycine--tRNA ligase
                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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PROSITE; PS50861; AA_TRNA_LIGASE_II_GLYAB; 1.

Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, Z99117; CAB14468.1; --
SubtiList; BG11658; Jtys.
SubtiList; BG11658; Jtys.
InterPro, IPR00231; tRNA_Synt_2f.
Pfam; PF02092; tRNA_Synt_2f; 1.
PRINTS; PR01045; TRNASYNTHGB.
                           TIGRFAMS; TIGRO0211; glyS; 1.

PROSITE; PS50861; AA_TRNA_LIGASE_II_GLYAB; 1.

Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase;
                                                                             Pfam; PF02092; tRNA_synt_2f; :
PRINTS; PR01045; TRNASYNTHGB.
                                                                                                                                 EMBL; AE000775; AAC07870.1; -.
                                                                                                                                                                                                                                                                                                                                                                      Nature 392:353-358(1998).
-!- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                               Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V., The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLYS OR AQ_2141.
Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYGB_AQUAE
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                                                                                                                                                               or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Aquificae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98196666; PubMed=9537320;
                                                                                                InterPro; IPRO02311; tRNA_synt_2f.
Pfam; PF02092; tRNA_synt_2f; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         567
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                                                                                                                                                                                                                                                                                                                                               + glycyl-trna(Gly).
SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS
                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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               proteome
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Pred. No. 0.00027;
1; Mismatches 45
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7FFEF7A8F552E3DB CRC64;
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                               ATP-binding
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16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                             TIGRFAMS; TIGR00211; glyS; 1.
PROSITE; PS50861; AA_TRNA_LIGASE_II_GLYAB; 1.
Aminoacyl-trNA_synthetase; Protein biosynthesis; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     halodurans and genomic sequence comparison with Bacillus Nucleic Acids Res. 28:4317-4331(2000).
-!- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) - AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glycyl-tRNA synthetase beta chain (EC 6.1.1
                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                           InterPro; IPR002311; trNA_synt_2f.
Pfam; PF02092; trNA_synt_2f; 1.
                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takami H., Nakasone K., Takaki Y., Maeno G., S
Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus halodurans.
Bacteria; Firmicutes;
NCBI_TaxID=86665;
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                                                                                                                                                                                Complete proteome
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                                                                                                                                                                                                                                                                                           EMBL; AP001511; BAB05090.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete genome sequence of the alkaliphilic bacterium
                                            564 VFKKAKLLVSKVNTPEFKELVEGLSRVTNIAGKAEKNVA-INPDLFEKEEERVLYEAYVQ 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 607 KSPL-ELLPLKEYIDKFFDNVKVMAEDEKIRNNRISLLKRVENLFRTFGD
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SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY)
VFKQ------LPEAAALAAANKRVQNLLKKADAALGEVNESLLQQDEEKALYAAAQG 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glycyl-tRNA(Gly)
                                                                                                        l Similarity
35; Conserv
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                                                                                                                                                                   693 AA;
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                                                                                                                                                                77833 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                        26;
                                                                                                           Score 137; Ub 1,
No. 0.00034;
                                                                                                    Pred. No. 0.006; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 137; DB 1; Pred. No. 0.00032;
                                                                                                                                                                   30F9919712105754 CRC64;
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6.1.1.14)
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                                                                                                                                   Length 693;
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                                                                                                                                                                                                ATP-binding
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Best Local 9
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Q55690;
Q1-NOV-1997
Q1-NOV-1997
Q1-NOV-1997
16-OCT-2001
G1YCY1-TRNA;
                           SYGB_BUCAI
P57235;
16-OCT-2001
16-OCT-2001
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLYS OR SLR0220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome."; DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              beta chain)
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PROSITE; PS50861; AA_TRNA_LIGASE_II_GLYAB; 1.

Aminoacy1-trNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002311; tRNA_synt_2f.
Pfam; PF02092; tRNA_synt_2f; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96127529; PubMed=8590279;
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1148;
      Glycyl-tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR01045; TRNASYNTHGB.
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                                                                                                                                                                                                                                                                                                                                                                                                                   633
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SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         + glycyl-tRNA(Gly)
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                                                                                                                                                                                                                                                                                                    ELRQNRLNLLGLIRNYALILGDFGAI 718
                                                                                                                                                                                                                                                                                                                                                       AVKONRLNLLNRLAEQMNAVADIALL 124
                                                                                                                                                                                                                                                                                                                                                                                                                LVQDSEKAVYQALLAIYPKAVEVQESRDYETLVNALHELAPTVAEFFDGPDSVLVMAEND 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
31; Conserv
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
synthetase beta chain (EC 6.1.1.14) (Glycine--tRNA ligase
(Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
synthetase beta chain (EC 6.1.1.14) (Glycine--tRNA ligase
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36.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 131.5; DB 1;
Pred. No. 0.001;
4; Mismatches 38;
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Search completed: December Job time: 4.06657 secs
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Best Local S
Matches 32
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Nature 407:81-86(2000).
-i- CATALYTIC ACTIVITY: ATP + glycine + trna(Gly) = AMP + diphosphate
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MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera
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Pfam; PF02092; tRNA_synt_2f; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed.
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-!- SUBUNIT: TETRAMER (BY SIMILARITY).
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PROSITE; PS50861; AA_TRNA_LIGASE_II_GLYAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01045; TRNASYNTHGB.
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Q9jvq7 neisseria m
Q51114 neisseria m
Q51213 ralstonia s
Q8y213 ralstonia s
Q9i7b8 pseudomonas
Q8xdn7 escherichia pe
Q8z9y7 yersinia pe
Q8z196 salmoneila
Q8z2b3 salmoneila
Q9f730 pseudomonas
Q9f326 neisseria m
Q8uhn6 agrobacteri
Q9gk01 brucella me
Q9cgk0 lactococcus
Q97pw6 streptococc
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ALIGNMENTS

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Query Match 96.2%; Score 575; DB 16; Length 687; Best Local Similarity 96.0%; Pred. No. 5.6e-39; Matches 121; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	Aminoacyi-tRNA synthetase; Complete proteome. SEQUENCE 687 AA; 74573 MW; 616BCBDD76A3D4FB CRC64;	TIGRFAMS; TIGR00211; glyS; 1.	PRINTS; PRO1045; TRNASYNTHGB.	INCEFFTO; IPROUZSII; CKNA_SYNT_ZF. Pfam: PFO2092: tRNA_SYNT_2f: 1.	TIGR; NMB1930; -	EMBL; AE002541; AAF42259.1;	Science 287:1809-1815(2000).	MC28. " мС28	, `	Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,	Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,	(E)	Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,	Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,	.J.,	Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,	MEDLINE=20175755; PubMed=10710307;	STRAIN=MC58 / SEROGROUP B;	SEQUENCE FROM N.A.	[1]	\Box		a moningitidic (concerns	beta	(TrEMBLrel. 21, Last	(TrEMBLrel, 15,	01-001-2000 (TrEMBLrel. 15, Created)	COTYCG: PRELIMINARY; PRT; 66/ AA.		RESULT 1

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Q9JW67;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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EMBL; AL162753; CAB83815.1; -.
EMBL; AL162753; CAB83815.1; -.
InterPro; IPR002311; tRNA_Synt_2f.
Pfam; PF02092; tRNA_Synt_2f; 1.
PRINTS; PR01045; TRNASYNTHOB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMS; TIGR00211; glyS; 1. Aminoacyl-tRNA synthetase; LiseQUENCE 687 AA; 74650 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      meningitidis 22491."
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MEDLINE=20222556; PubMed=10761919;
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STRAIN=Z2491 / SE
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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Q8Y213;
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SEQUENCE
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                         Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415.497-502(2002).
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable 91ycy1-tRNA synthetase beta chain protein
GLYS OR RSC0524 OR RSC04944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-126E
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Bacteria; Proteobacteria; beta subdivision; Ralst
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                                                                                                                                                                                                                                                                                         InterPro; IPR002311; tRNA_synt_2f.
Pfam; PF02092; tRNA_synt_2f; 1.
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       Conservative
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97.7%;
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           19;
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Pred.
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Pred. No. 2.
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           Mismatches
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.2e-26;
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                                                5e-17
                                                                                  DB 16;
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               39;
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                                                                                      697;
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                                                                                                                                                                                                                   RESULT
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20 STRAIN-ATCC 15692 / PAO1;

22 STRAIN-ATCC 15692 / PAO1;

23 X MEDLINE-20437337; PubMed-10984043;

24 A Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

25 A Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

26 A Garber R.L., Goulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

27 A Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

28 A Smith K.A., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

27 "Complete genome sequence of Pseudomonas aeruginosa PAO1, an

28 Opportunistic pathogen.";

29 Nature 406:959-964(2000).

20 EMBL; AE004440; AA603398.1; -.

20 EMBL; AE004440; AA603398.1; -.
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Best Local S
Matches 61
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Q91788;
Q1-MAR-2001;
Q1-MAR-2001;
Q1-JUN-2002;
O8XDN7:
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glycine tRNA synthetase, beta subunit.
GLYS OR Z4983 OR ECS44442.
                                                                                                                                                               Q8XDN7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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SEQUENCE 684 AA; 73973 MW; 74144075010F0BE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002311; tRNA_synt_2f. Pfam; PF02092; tRNA_synt_2f; 1.
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Last sequence update)
Last annotation update)
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0; Mismatches
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Pred. No. 6.2
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Best Local
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Q8Z9W7;
01-MAR-2002 (TIEMBLITE1. 2
01-MAR-2002 (TIEMBLITE1. 2
01-JUN-2002 (TIEMBLITE1. 2
SEQUENCE FROM N.A.
STRAIN-CO-92 / BIOVAR ORIENTALIS;
MEDLINE-21470413; PubMed-11586360;
Parkhill J. Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
                                                                                                                                      Glycyl-tRNA synthetase GLYS OR YPO4071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Appodaca J., Anatrharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                               Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature
[2]
                                                                                       NCBI_TaxID=632;
                                                                                                                             Yersinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMS; TIGR00211; glyS; 1.
Aminoacyl-tRNA synthetase; Complete
SEQUENCE 689 AA; 76813 MW; 3F9BS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Welch R.A., Blattner F.R.;
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48.0%;
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                                                                                                               gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                Last sequence update)
Last annotation update)
subunit (EC 6.1.1.14).
                                                                                                                                                                                        Created)
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Pred. No. 1.3
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retwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
DR EMBL; AJ414100; CAC93524.1; -.
DR InterPro; IFR002311; tRNA_synt_2f.
DR pfam; PF02092; tRNA_synt_2f; 1.
DR pfam; PF02092; tRNA_synt_2f; 1.
DR pfam; PF02092; tRNA_synt_BB.
DR prints; PR01045; TRNASYNTHGB.
DR pfam; PF02092; tRNA_Synt_BB.
DR prints; PR01045; TRNASYNTHGB.
DR prints; PR010411; 91yS; 1.
KW Aminoacy1-tRNA synthetase; Ligase; Complete
30 SEQUENCE 689 AA; 76204 Mm<sup>2</sup>.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glycine tRNA synthetase, beta subunit (EC 6.1.1.14).
GLYS OR STM3655.
                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGR00211; glyS; 1.
Aminoacyl-tRNA synthetase; LissEQUENCE 689 AA; 76452 MW;
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InterPro; IPR002311; tRNA_synt_2f.
Pfam; PF02092; tRNA_synt_2f; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
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KIAAAVAEGNERTALSELASVKPQVDAFFDGVMYMAEDAAVKQNRLNLLNRLAEQMNAVA 119
                                                                                                         LQAVAVFKQLPEAAALAAANKRVQNLLKKADAALGE-VNESLLQQDEEKALYAAAQGLQP 59
                                                              MKAYSHFRTLEEASALAAANKRYSNILAKATEPLNDIVHASVLKEAAEIELARHLVVLRD 623
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fw; 5734C31C5223123F CRC64;
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Pfam; PF02092; tRNA_synt_2f; 1.
PRINTS; PR01045; TRNASYNTHGB.
TIGRFAMS; TIGR00211; g1ys; 1.
Aminoacyl-tRNA synthetase; Ligase;
SEQUENCE 689 AA; 76645 MW; A93C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
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01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
EMBL; AL627281; CAD07973.1; -.
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O9F730;

O1-MAR-2001 (TrEMBLrel. 16,

O1-MAR-2001 (TrEMBLrel. 16,

O1-JUN-2001 (TrEMBLrel. 17,
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                                     GlyS-like protein (Fragment). Pseudomonas fluorescens.
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         Pseudomonas
                          Bacteria; Proteobacteria;
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(TrEMBLrel. 21, Last annotation
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ta subunit (EC 6.1.1.14)
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Matches 51
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Q8UHN6;
Q8UHN6;
01-JUN-2002
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Q932S6;
Q1-DEC-2001
Q1-DEC-2001
Q1-JUN-2002
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MEDLINE-21467954, PubMed-11583844;
MEDLINE-21467954, PubMed-11583844;
Zhu P., Klutch M.J., Tsai C.-M.;
"Genetic Analysis of Conservation and Variation of Lipooligosaccharide "Genetic Analysis of Conservation and Variation of Lipooligosaccharide Expression in Two L8-Immunotype Strains of Neisseria meningitidis.";
FEMS Microbiol. Lett. 203:173-177(2001).
EMBL; AF355193; AAL12843.1; -.
EMBL; AF355194; AAL12843.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laue B.E., Jiang Y., Chhabra S.R., Jacob S., Stewart Hardman A., Downie J.A., O'Gara F., Williams P.; "The biocontrol strain Pseudomonas fluorescens F113 Rhizobium small bacteriocin, N-(3-hydroxy-7-cis-
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=M978, AND F
                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis.
Bacteria; Proteobacteria;
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acylhomoserine lactone synthase.";
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MBL; AF286536; AAG30824.1; -..

iterPro; IPR002311; tRNA_synt_2f.

fam; PF02092; tRNA_synt_2f; 1.
                                                                                            87 FFDGVMVMAEDAAVKQNRLNLLNRLAEQMNAVADIALLGE 126
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                                                                                                                                                                                40 AA; 4392 MW;
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(TrEMBLrel.
                                                                                                                                  Conservative
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                         PRELIMINARY;
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100.0%;
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21,
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                                                                                                                                             Score 193;
Pred. No.
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Pred. No. 7
                                                                                                                                                                                E41CA1A42B65A187 CRC64;
                         PRT;
                                                                                                                                                                                                                                                                                                                                     subdivision; Neisseriaceae; Neisseria.
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                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                  sequence update)
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                                                                                                                                          3.3e-09;
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Q986B5
ID Q9
AC Q986B7
DT 01
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Best Local
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Q986B5;
Q1-OCT-2001
Q1-OCT-2001
Q1-JUN-2002
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"Genome Seguence of the County of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-21608550; PubMed-11743193;

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo L.,

Chen Y., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Gordon

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Gordon

Raymond C., Rouse G., Saenphimmachak C., W. Z., Romero P., Gordon

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

Nester F. W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE009032; AAL41660.1; -
EMBL; AE007998; AAK86451.1; -
Aminoacyl-tRNA synthetase; Complete
SEQUENCE 717 AA; 78713 MW; 94F26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TYEMBLrel. 21, Last sequence update)
01-JUN-2002 (TYEMBLrel. 21, Last annotation update)
Glycyl-trna synthetase, beta chain.
GLYS OR ATU0644 OR AGR_C_1144.
                                                                       Phyllobacteriaceae; NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the plant Agrobacterium tumefaciens C58. Science 294 2323-2328 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 294:2317-2323(2001).
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   SEQUENCE FROM N.A
                                                                                                                                                       Bacteria;
                                                                                                                                                                                       Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                                   MLR7435
                                                                                                                                                                                                                                                                   Glycyl-tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nester E.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                       Proteobacteria;
                                                                                                                                                                                                                                                                   l (TrEMBLrel. 18, C. l (TrEMBLrel. 18, L. 2 (TrEMBLrel. 21, L. synthetase, beta
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Mesorhizobium.
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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2e-07;
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Matches 45
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MEDLINE=21082930; PubMed=11214968;

KÅDEKO T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Kabneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Kabneko T., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Watanabe A., Idesawa C., Kohara M., Matsumoto M., Matsuno A., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Kiyokawa C., Kohara M., Shimpo S., Sugimoto M., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Tabata S.;
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EMBL; AP00301; BAB535381; -.

InterPro; IPR00231; tRNA_Synt_2f.

Pfam; PF02092; tRNA_Synt_2f; 1.

PRINTS; PR01045; TRNASYNTHOB.
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O1-MAR-2002 (TrEMBLrel. 20,

O1-JUN-2002 (TrEMBLrel. 21,

O1-JUN-2002 (TrEMBLrel. 21,

Clycyl-tRNA synthetase beta
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Aminoacyl-tRNA synthetase; Complete proteome.
SEQUENCE 718 AA; 78610 MW; 6664029CFFA0C689 CRC64;
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PfAm; PF02092; tRNA_synt_2f; 1.
TIGRFAMs; TIGR00211; glyS; 1.
Ligase; Complete proteome.
SEQUENCE 780 AA; 85795 MW; 279
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MEDLINE=20020109; PubMed=11756688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brucella melitensis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haselkorn R., Kyrpides N., Overbeek R.; "The genome sequence of the facultative Brucella melitensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brucellaceae; Brucella.
NCBI_TaxID=29459;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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1 LQAVAVFKOLPEAAALAAANKRVQNLL----KKADAALGEVNESLLQQDEEKALYAAAQG
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                                                                                                                                            1 Similarity
45; Conserv
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                                                                                                                                                                                           28.9%;
                                                                                                                                            22;
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Last sequence update)
Last annotation update)
chain (EC 6.1.1.14).
                                                                                                                                            Score 173; DB 16;
Pred. No. 4.9e-06;
2; Mismatches 55;
                                                                                                                                                                                                                                                                                                                       27947D756B21FE80 CRC64;
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Best Local S
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A Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
A Weissenbach J., Ehrlich S.D., Sorokin A.;
The complete genome sequence of the lactic acid bacterium
The complete genome sequence of the lactic acid bacterium
T lactis ssp. lactis IL1403.";
T lactis ssp. lactis IL1403.";
T genome Res. 11:731-753(2001).
R EMBL; AE006341; AAK05194.1; -.
R InterPro; IPR002311; tRNA_synt_2f.
R Pfam; PF02092; tRNA_synt_2f; 1.
R Pfam; PF02092; tRNA_SYNTHGB.
R PFINVTS; PR01045; TRNASYNTHGB.
R PFINVTS; PR01045; TRNASYNTHGB.
R PTIGREAMS; TIGR00211; g195; 1.
R Aminoacyl-tRNA synthetase; Complete proteome.
SEQUENCE 673 AA; 75717 MW; 99CF078804DAE69E CRC64;
                                                                                                                                                                                                                                                                                               Matches
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glycyl-tRNA synthetase beta chain (EC 6.1.1.14).
GLYT OR LL1096.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobac
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nes 38; Conserv
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                                                                                                                                               NLVKKA-KDIKEINPTLFEEDAEEALYNVVISLQNQWTYMPGEEKFRAIVHSLA---PAI 630
                                                                                                                                                                                                                    NLLKKADAALGEVNESLLQQDEEKALYAAAQGLQPKIAAAVAEGNFRTALSELASVKPQV 84
ETFFESVMVMAEDLSVRDNRIALLSEVVALTSVMADFSLI
                                                                    DAFFDGVMVMAEDAAVKQNRLNLLNRLAEQMNAVADIALL
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Pred. No. 2.2e
21; Mismatches
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2.2e-05;
hes 37;
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Title:
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Maximum Match 1008
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Maximum DB seq
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       A_Geneseq_101002:*

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2: /SIDS2/gcgdata/g
3: /SIDS2/gcgdata/g
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length: 2000000000
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SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT: *
10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT: *
11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *
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Copyright (c) 1993 - 2002 Compugen Ltd.
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length DB	ength		ID	Description
1	1823	100.0	348	17	AAR91311	N. gonorrhoeae glv
2	1820	99.8	348	18	AAW06576	Neisseria polyglyc
ω	1709	93.7	346	23	AAU72923	Neisseria meningit
4.	1049	57.5	337	17	AAR91314	N. gonorrhoeae gly
տ	1046	57.4	337	18	AAW06579	Lipo-oligosacchari
σ.	254.5	14.0	274	22	AAG90151	C qlutamicum prote
7	244	13.4	50	20	AAW89330	Neisseria meningit
8	227	12.5	278	21	AAY68976	CpslK protein whic
9	226.5	12.4	334	21	AAY68963	Cps2K protein whic
10	225	12.3	298	22	AAB96313	Putative glycosylt

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
175	175	175	177	177	179	179	181	183	185.5	189.5	190	190.5	191.5	191.5	193.5	193.5	194.5	195	200	200.5	205	207.5	207.5	208.5	208.5	210	210	210	210	211	14	14	217.5	17
	9.6										10.4	•	•	•	•	•	10.7	•	•	11.0	•	11.4		11.4		11.5	1.			11.6		11.8		11.9
281	270	270	322	322	389	345	328	332	311	350	270	302	674	674	268	268	322	301	702	327	329	336	336	972	972	965	965	965	322	332	316	316	324	324
19	23	19	21	21	21	22										21	21	21	21	23	22	21	21	21	20	23	23	21	21	22	21	21	18	18
	ABP54655	123	377	407	AAY97202	014	AAY81720	AAY68962	ABB52989	AAB96485	AAY97203	AAY97213	ABP54656	AAW61238	AAY43795	AAY54093	AAY68975	AAY97206	AAY96212	ABB48565	AAB47427	AAY43800	AAY54098	AAY43099	AAY06212	AAM47336	AAM47335	AAY96213	97	J	377	407	217	AAW14078
	S. pneumoniae SP11	Streptococcus pneu	Amino acid sequenc	Enzyme EPS7 which	Campylobacter jeju		Streptococcus pneu	Cps2J protein whic	Escherichia coli p	.Putative glycosylt	Campylobacter jeju	Campylobacter jeju	S. pneumoniae SP11	Streptococcus pneu	cid s			Campylobacter jeju	P. multocida hyalu	Ľ.		icid s	Enzyme EPSM involv	OJ			steurella m	-	ם	Lact	cid	<u>_</u>	.thermophilus	S.thermophilus exo

ALIGNMENTS

RESULT 1 AAR91311

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Nucleic acids encoding glycosyl transferase(s) - used in the diagnosis of infection with Neisseria and for the biosynthesis oligo:saccharide(s) {\bf r}
                                             WPI; 1996-200924/20.
N-PSDB; AAT14061.
                                                                                                                                                                                                                                                                    N. gonorrhoeae glycosyltransferase LgtA.
                                                                               Gotschlich EC;
                                                                                                   (UYRQ ) UNIV ROCKEFELLER.
                                                                                                                          26-SEP-1994;
                                                                                                                                                                   04-APR-1996.
                                                                                                                                                                                         W09610086-A1.
                                                                                                                                                                                                              Neisseria gonorrhoeae strain F62
                                                                                                                                                                                                                                     vaccine.
                                                                                                                                                                                                                                             Glycosyltransferase; lipo-oligosaccharide; lgt gene; LOS locus;
                                                                                                                                                                                                                                                                                         09-JUL-1996
                                                                                                                                                                                                                                                                                                                AAR91311;
                                                                                                                                                                                                                                                                                                                                     AAR91311 standard; Protein; 348 AA.
                                                                                                                                              25-SEP-1995;
                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                        94US-0312387
                                                                                                                                              95WO-US12317
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Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                    Дb
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 Glycosyltransferases (AAR91311-15) are products of the lgt locus (AAR14061) of Neiserria gonorrhoeae strain F62. Glycosyltransferase LgtA (AAR91311) can be obtd. by expression of the lgtA coding sequence in recombinant host cells. A method for adding GalNAC or GlcNAc betal-3 to Gal comprises contacting a reaction mixture contg. activated GalNAc or GlcNac to an acceptor moiety comprising a Gal residue in the presence of LgtA. Oligosaccharides can be produced that, when attached to non-toxic lipids, are useful for Neisseria vaccine prepn. Blood group core oligosaccharides, and mimics of lacto-N-neotetraose, gangliosides and saccharide portions of globoglycollpids can also be produced using the enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Fig
                                                                                                                                                                                                                                                                                                                      AAW06576 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                      21-MAR-1997
                                                                                                                                                                                                      N-acetylgalactosaminyl transferase;
                                                                                                                                                                                                                                             Neisseria
                                                                           07-JUN-1995;
                                                                                                                             19-DEC-1996
                                                                                                                                                                             Neisseria
                                                                                                                                                                                                                    Polyglycosyltransferase; N-acetylglucosaminyl transferase
                                                (NEOS-) NEOSE TECHNOLOGIES INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSGAWLDFAADGRWRRLFTLRQYFGILYRLIKNRRQARSDSAGKEQEI 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                 QKTARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEKDLPEEDFERARRFLYQCFKRTDTP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGGLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKYRLHANQVSSKHSVRQHEIAQGI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IAMGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNPIHNNTMIMRRSVI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IAMGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNPIHNNTMIMRRSVI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                     QKTARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEKDLPEEDFERARRFLYQCFKRTDTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGGLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKYRLHANQVSSKHSVRQHEIAQGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity
348; Conserv
                          SL,
                                                                                                                                                                             gonorrhoeae ATCC 33084.
                                                                                                                                                                                                                                           polyglycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 AA;
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                                                                                                                                                                                                                                                                       (first entry)
                           Johnson KF,
                                                                            95US-0478140
                                                                                                    96WO-US08323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81pp;
                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                           Roth
                                                                                                                                                                                                                                                                                                                         348
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                        lipo-oligosaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 17;
3.2e-184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 348;
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RESULT 3
AAU72923
ID AAU7
XX AAU7
AC AAU7
XX Per 12-M
XX Meni
KW Infe
XX Meis
XX Neis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A novel polyglycosyltransferase (PGTase) (AAW06576) from Neisseria gonorrhoeae ATCC 33084 catalyses the stereospecific conjugation of 2 specific activated saccharide units (e.g. UDP-GalNac, UDP-GalNac, UDP-Gal) to specific acceptors having a galactose moiety at a non-reducing end. It is the first PGTase reported to be capable of transfer of more than one different saccharide moiety. The PGTase is encoded by nucleotides 445-1488 of a lipo-oligosaccharide gene (AAT49230). It can be produced in transformed host cells and used oligosaccharida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transfer of at least 2 saccharide units using poly:glycosyl:transferase - isolated from N. gonorrhoeae, catalyses the addition of both GlcNac and GalNac di:saccharide(s) units to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT49230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oligosaccharide prodn.
                                                                                                                                                                                                                                                                               AAU72923 standard;
                                                                                                                                              Meningitis; virulence; gene;
infection; Gram-negative bact
                                                                                                                                                                                                                    12-MAR-2002
                             08-MAY-2001;
                                                                                      WO200185772-A2
                                                                                                                 Neisseria meningitidis
                                                                                                                                                                                        Neisseria meningitidis virulence protein
                                                                                                                                                                                                                                                                                                                                                     301
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                                                                                                                                                                                                                                                                                                                                                     PSGAWLDFAADGRMRRLFTLRQYFGILYRLIKNRRQARSDSAGKEQEI 348
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347; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                      (first entry)
                               2001WO-GB02003
                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.8%;
99.7%;
                                                                                                                                               bacteria; antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1820; DB 18;
Pred. No. 6.6e-184;
1; Mismatches 0;
                                                                                                                                                                antibacterial; vaccine; veterinary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 18;
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08-MAY-2000; 2000GB-0011108

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RESULT 4
AAR91314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reisseria meningitidis including virulence genes, or a related molecule having a 40% sequence similarity at the peptide or nucleotide level in a Gram-negative bacterium, or its functional fragment, for therapeutic or diagnostic use. (I) and (II) are useful in the manufacture of a medicament for treating or preventing a condition (e.g., meningitis) associated with infection by Neisseria or Gram-negative bacteria. The product is useful for veterinary treatment and in a screening assay for the identification of an antimicrobial drug. The vaccines have prophylactic applications. AAU72911-AAU73014 represent N. meningitidis virulence proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 200
N-PSDB;
 W09610086-A1
                                                                                                                                                                    AAR91314 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 60-61; 423pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptide encoded by operon including virulence genes of meningitidis, useful as vaccine component for treating or meningitis and for identifying antimicrobial drug -
                         Neisseria
                                                                                         N. gonorrhoeae
                                                                                                                   09-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MQPLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-066593/09
DB; AAS97208.
                                                                                                                                                                                                                                      PAGAWLDFAADGKMRRLFTMRQYFGILHRLIKNRRQARSDSAGKEQEI 346
                                                                                                                                                                                                                                                                                                      QKTARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEKDLPEEDFERARRFLYQCFKRTDTP
                                                                                                                                                                                                                                                                                                                                                        DGGLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKYRLHANQVSSKHSVRQHEIAQGI 240
                                                                                                                                                                                                                                                                                                                                                                                              IAMGAWLEVLSEEKDGNRLARHHRHGKIWKKPTRHEDIADFFPFGNPIHNNTMIMRRSVI
                                                                                                                                                                                                                                                                                                                                                                                                            IAMGAWLEVLSEEKDGNRLARHKHGKIWKKPTRHEDIAAFFPFGNPIHNNTMIMRRSVI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                  KILAQAQNSGLIPSLNIGLDELAKS--GMGEYIARTDADDIAAPDWIEKIVGEMEKDRSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KILAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQPLVSVLICAYNVEKYFAQ$LATVVNQTWRNLEILIVDDGSTDGTLAIAKDFQKRDSRI
                                                                                                                                                                                                                                                              PSGAWLDFAADGRMRRLFTLRQYFGILYRLIKNRRQARSDSAGKEQEI
                                                                                                                                                                                                                                                                                       QKTARNDFLQSMGFKTRFDSLEYRQIKAVAYELLEKHLPEEDFERARRFLYQCFKRTDTP
                                                                                                                                                                                                                                                                                                                                            DGGLRYNTERDWAEDYQFWYDVSKLGRLAYYPEALVKYRLHANQVSSKYSIRQHEIAQGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                         gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 AA;
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                                                                                                                   (first
                                                                                        glycosyltransferase LgtD
                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.7%;
94.0%;
                                                              lipo-oligosaccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                      337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1709; DB 23;
Pred. No. 3.8e-172;
1; Mismatches 8;
                                                                                                                                                                      A
                                                              lgt
                                                              gene;
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or preventing
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RESULT 5
AAW06579
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding glycosyl transferase(s) - used in the diagnosis of infection with Neisseria and for the biosynthesis oligo:saccharide(s)
 Lipo-oligosaccharide
                                    21-MAR-1997
                                                                                                   AAW06579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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les 214; Conservative
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                                                                                                                                                                                                                                                                           QKTARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEKDLPEEDFERARRFLYQCFKRTDTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KILAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSI 120
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                                                                                                                                                                                    SLTDLLDFLTDRVMRKLFAAPQYRKILKKMLR 330
                                                                                                                                                                                                                                                   KEEIRAGYWKAAGIAVGADCLNYGLLKSTAYALYEKALSGQDIGCLRLFLYEYFLSLEKY
                                                                                                                                                                                                                                                                                                                      DGGLRFDPAYIHAEDYKFWYEAGKLGRLAYYPEALVKYRFHQDQTSSKYNLQQRRTAWKI
                                                                                                                                                                                                                                                                                                                                                                                      IAMGAWLEVLSEENNKSVLAAIARNGAIWDKPTRHEDIVAVFPFGNPIHNNTMIMRRSVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIISNPRNLGFIASLNIGLDELAKS--GGGEYIARTDADDIASPGWIEKIVGEMEKDRSI
                                                                                                                                                                                                                    PSGAWLDFAADGRMRRLFTLRQYFGILYRLIK 332
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                                                                                                   standard;
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64.5%;
gene-encoded
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Pred. No. 2.
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Best Local Similarity
Matches 213; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2E-F; 38pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transfer of at least 2 saccharide units using poly:glycosyl:transferase - isolated from N. gonorrhoeae, cataly: the addition of both GlcNac and GalNac di:saccharide(s) units to
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                                                      AAG90151;
                                                                                  AAG90151
                             26-SEP-2001
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                                                                                                                                                                                                                                                                     DGGLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKYRLHANQVSSKHSVRQHEIAQGI 240
                                                                                                                                                                                                                                                                                                                            IAMGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNPIHNNTMIMRRSVI 180
                                                                                                                                                                                                                                                                                                              IAMGAWLEVLSEENNKSVLAAIARNGAIWDKPTRHEDIVAVFPFGNPIHNNTMIMRRSVI
                                                                                                                                                                                                                                                                                                                                                                 RIISNPRNLGFIASLNIGLDELAKS--GGGEYIARTDADDIASPGWIEKIVGEMEKDRSI 118
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                                                                                                                                                                                                                                                                                                                                                                                                                     LQPLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGRI 60
                                                                                                                                                  SLTDLLDFLTDRVMRKLFAAPQYRKILKKMLR 330
                                                                                                                                                                           PSGAWLDFAADGRMRRLFTLRQYFGILYRLIK 332
                                                                                                                                                                                                    KEETRAGYWKAAGTAVGADCLNYGLLKSTAYALYEKALSGQDIGCLRLFLYEYFLSLEKY
                                                                                                                                                                                                                              QKTARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEKDLPEEDFERARRFLYQCFKRTDTP
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                                                                                  standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the specification.
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                             (first entry)
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                                                                                  Protein;
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Pred. No. 6.1e-102;
4; Mismatches 83;
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Query Match
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coryneform bacterium; amino organic acid synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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219
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DB; AAH65370.
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                                                                                                                                                                                                     IIAMGAWLEVLSEEKDGNRLARHHKHGKIWKK----PTRHEDIAAFFPFGNPIHNNTMIM 175
                                                                                                                                                                                                                                                                                IKILAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRS 119
                                                                                                                                                                                                                                                                                                                                     PLISVVIPTIAYDEYCSQSIKSVCEQNYENWQIVLVLDG----
                                                                                                                                                                                                                                                                                                                                                                              PLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKD---FQKRDSR 59
                                                                                 RKQVVEQIGG--YSLEMTRSQDYELFLRLSKIGAIGYLDESLSSYRIHGGQHSRKTSPFK
                                                                                                                        RRSVID--GGLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKYRLHANQVSSKHS---
                                                                                                                                                                                                                                                   IKIVEQKIRQGTPTSLNNGIK-----ASDGQLIARLDSDDLAAPSRLSKQEEFLRNHPY 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent Office
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleotides derived from Coryneform bacteria, for identi-
bint of a gene, measuring expression of a gene, analysim
profile or pattern of a gene and identifying homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274 AA;
                                       -VRQHEIAQGIQKT-ARNDFL 249
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Senoh A, Ik
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2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ikeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ando
da M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                          49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 254.5; DB Pred. No. 3e-18; 9; Mismatches 9
                                                                                                                                                                    HGKIFGQSADLPT-SQDIRQILLVKNPIIHSSVMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S, Hayashi M,
Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IJ
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                                                                                                                                                                                                                                                                                                                                                                                                                          91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
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                                                                                                                                                                                                                                                                                                                                         -APIKDVPQWVKEHER 59
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274;
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                                                                                                                                                                                                                                                                                                                                                                                                                          47;
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RESULT 8
AAY68976
ID AAY6
XX
AC AAY6
XX
DT 30-M
XX
XX
DE Cps1
XX
KW Caps
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AAW89330
                                                                                                                                                                                            Вþ
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                                                                                                                                                                                                                                                                                                              A method has been developed of expressing a glycosyltransferase in a C host cell. The method comprises introducing into the host cell a nucleic acid encoding the glycosyltransferase and incubating the host cell under conditions appropriate for expression of the glycosyltransferase, where the host cell substantially lacks a protease that cleaves polypeptides between two consecutive positively charged amino acid residues. The glycosyltransferase can be used in in vitro production of collososyltransferase can be used in in vitro production of collososyltransferase can be used in in contential therapeutic agents for use in the manipulation of cell-cell recognition events, particularly adhesion of bacteria and viruses to mammalian cells and leukocyte-centodial cell interaction through selectins in inflammation. The method provides more readily recoverable active glycosyltransferases. The present sequence represents a C-terminal peptide from Neisseria
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                               Query Match
Capsular gene cluster; serotype 1; polysaccharide biosynthesis;
                          CpslK protein which has glycosyltransferase activity.
                                                           30-MAY-2000
                                                                                        AAY68976;
                                                                                                                    AAY68976 standard;
                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                         meningitidis lgtA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 8; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expressing high levels of glycosyltransferases - comprises use either host cells deficient in proteolytic enzymes or modified glycosyltransferase genes deleted in a proteolytic recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycosyltransferase;
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                                                                                                                                                                                                                      286 ARRFLYQCFKRTDTPPSGAWLDFAADGRMRRLFTLRQYFGILYRLIKNR 334
                                                                                                                                                                                                                                                   Local Similarity
nes 45; Conserv
                                                                                                                                                                                            N
                                                                                                                                                                                         meningitidis; lgtC; lgtB; beta-1,4-galactosyltransferase;
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                                                        (first entry)
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                                                                                                                    Protein;
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                                                                                                                                                                                                                                                                 Score 244; DB 20;
Pred. No. 3.1e-18;
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                                                                                                                                                                                                                                                                                                                                         invention
                                                                                                                                                                                                                                                                               20;
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RESULT 9
AAY68963
ID AAY6

AAY68963

standard;

Protein;

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Best Local S
Matches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus suis serotype 1. The genes in this cluster are involved in polysaccharide biosynthesis of capsular components and antigens. The proteins have glycosyltransferase activities (CpsIE, CpsIG, CpsII, CpsIII, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombinant production of the proteins. The proteins for producing antigens that can be used in vaccines, or eradicating a Streptococcal disease, in humans or e.g. against S. suis in pigs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid containing the capsular gene cluster of Streptococcus suis, used for serotype-specific detection and to generate antigens or mutants for vaccination -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus suis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 4; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-195104/17.
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22-JUL-1998;
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   213
                                                                                                                   153
                                                                                                                                                                             184
                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                             125
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                                                                                                                                                                          LRYDTER-----DWAEDYQF------WYDVSKLGRLAYYPEALVKYRL
                                                                                                                                                                                                                                                                                                                                                 ISIIVPIYNVEKYLSKCIDSIVNQTYKHIEILLVNDGSTDNSEEICLAYAKKDSRIRYF- 65
                                                         HANQVSSKHSVRQHEIAQGIQ-KTARNDFLQSMGFK 255
                                                                                                                                                                                                                                      GYDRV------DASGHFLTAEPLPTNQAVLSGRNVCKKL
                                                                                                                                                                                                                                                                                                                                                                                                          QAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAMG 124
RENSITTS-SMTDHRFHCLLEFQNERMDFYESRGDK 247
                                                                                                                   LEADGHRFVVACNKLYKKELFEDFRFEKGKIHEDEYFTYRLLYELEKVAIVKECLYYYVD
                                                                                                                                                                                                                                                                                          AWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNPIHNNTMIMR-RSVIDGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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98EP-0202467.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 227; DB 21;
Pred. No. 2.5e-15;
0; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 278;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The proteins AAY68950-69 are encoded by the capsular gene cluster of Streptococcus suis serotype 2. The genes in this cluster are involved in polysaccharide biosynthesis of capsular components and antigens. The proteins are involved in regulation (CpsA), chain length determination (CpsB, CpsC), export (CpsC), and biosynthesis (CpsE, CpsF, CpsG, CpsH, CpsK). The capsule confers bacterium resistance to complement-mediated opsonophagocytosis. The gene cluster is used as a source of probes and primers for serotype-specific detection of S. suis and is also useful for recombinant production of the proteins. The proteins are then useful for producing antigens that can be used in vaccines, for controlling or eradicating a Streptococcal disease, in humans or animals, e.g. against S. suis in pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200005378-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 3; 144pp; English.
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22-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid containing the capsular gene cluster of Streptococcus suis, used for serotype-specific detection and to generate antigens or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAZ60929
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     221
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HANQV--SSKHSVRQHEIAQGIQKTARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEKDL
                                                           LEADGHRFVVAWNKLYKKELFEDFRFEKGKIHEDEYFTYRLLYELEKVAIVKECLYYYYD
                                                                                                                   AWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNPIHNNTMIMR-RSVIDGG 183
                                                                                                                                                                                                                                                                                                                                            QAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAMG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRIKILA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-195104/17.
                                                                                                                                                                                                                                                                                       KKENGGLSDARNYGISR-AK-----GDYLAFIDSDDFIHSEFIQRLHEAIERENALVAVA 116
                                                                                                                                                                                                                                                                                                                                                                                                       ISIIVPIYNVEQYLSKCINSIVNQTYKHIEILLVNDGSTDNSEEICLAYAKKDSRIRYF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccination
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98EP-0202467
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22.7%;
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 226.5;
Pred. No. 3.8
                                                                                                                   -----WYDVSKLGRLAYYPEALVKYRL
                                                                                                                                                                         -DASGHFLTAEPLPTNQAVLSGRNVCKKL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .8e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
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RESULT 10
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                                                                                                                                Matches
                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                           The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAH41233-7) and P. abyssi proteins. P. abyssi a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial
                                                                                                                                                                                   Sequence
                                                                                                                                                                                                             contains additional sequences as AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-126236/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Forterre P,
Querellou J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FR2792651-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hyperthermophilic archaeon; hyperthermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative glycosyltransferase, involved in cell wall biogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                    New nucleotide sequences isolated from proteins useful in industry -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB96313 standard;
 119
                                                                                                                                                                                                                                                  uses, since the proteins are stable at very high temperatures, 10 degrees centigrade.
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SIIAMGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNPIHNNTMIMRRS 178
                        YIRLKKNSGGPIARNIGIKK-AK-----GRFIALLDDDDEWLPHRLEVQVRKFENLGKEF
                                                  ILAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEME----KDR 118
                                                                                                     QPLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRIK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'RLIK-NRRQA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RENSITTSSMTDHRFHCLLE--FQNERMDFYESRG
                                                                            RPIVSVIIPTYNRANLLRRAIASVLNQKFKDFELIVVDDASTDNTPEVVESIE--DGRIR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KQLKQNKRLA
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                                                                                                                                                                                                                                      This patent is in the same patent family as WO200065062,
                                                                                                                                  65;
                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                          Pages 981-982; 1657pp; French.
                                                                                                                                                                                    298 AA;
                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thierry JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein; 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                             12.3%;
26.5%;
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                                                                                                                                52;
                                                                                                                                           Score 225; DB 22;
Pred. No. 4.6e-15;
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                                                                                                                                96;
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Matches
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                                                                                                                                                                                     probably a glycosyl transferase.

Novel exopolysaccharides can be produced by transforming lactic acid bacteria which produce exopolysaccharides with DNA encoding at least one enzyme from the eps operon. The new exopolysaccharides are useful for thickening drinks, liquid desserts, yoghurts, soups,
                                                                                                                                                                                                                                                      A chromosomal DNA sequence representing practically the whole eps (exopolysaccharide biosynthesis) operon from Streptococcus thermophilus strain Sfi6 (deposited as CNCM I-1590) was isolated. The sequence contained 14 open reading frames, one of which was located on the complementary strand. The present sequence is decoded from the epsH open reading frame. The EpsH protein is
                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                           Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                    DNA from lactic acid bacteria - exo-polysaccharide biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus thermophilus strain Sfi6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Exopolysaccharide biosynthesis; eps operon; lactic acid bacterium;
epsR; epsA; epsB; epsC; epsB; epsE; epsF; epsG; epsH; epsI; epsJ;
epsK; epsL; epsZ; CNCM I-1590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S.thermophilus exopolysaccharide biosynthesis enzyme EpsH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW14078;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-DEC-1996
                                                                                                                                                                          ice-creams, coffee creams, sauces, mayonnaise, etc
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            61
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                                                       MQPLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRI 60
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           KILAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVRQH 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CFKKAGLFDPRLSSSQDWDMWLRIARYYKFDYVDEIIAKYYVHGKQISFNMKKYIPGRER 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIDGGLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKYRLHANQVS---
                                      LKSLISIVIPVYNVEKYLEKCLQSVQNQTYNNFEVILVNDGSTDSSLSICEKFVNQDKRF 62
                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                         Pages 33-34; 42pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227
<u>:-</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stingele
                                                                                                                                                   324 AA;
                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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23.6%;
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                                                                                                        Score 217.5; DB 1
Pred. No. 3.2e-14;
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                                                                                                                     DB 18;
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                                                                                           Indels
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                                                                                                                     Length
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                                                                                                                     324;
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62

Local Similarity les 80; Conserv

Conservative

67;

Mismatches

103;

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RESULT 12
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Query Match
Best Local S
Matches 80
                                                                         encoded by the Rfbv ORF of the rfb cluster from Salmonella typhimurium and is probably a glycosyl transferase. The EPS are useful for thickening e.g. drinks, liquid desserts, yoghurts, soups, ice-creams, coffee creams, sauces, mayonnaise.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus thermophilus; operon; exopolysaccharide; synthesis; open reading frame; thickening; drink; liquid dessert; yoghurt; sauce; ice-cream; coffee cream; mayonnaise; glycosyl transferase.
                                                                                                                                        This sequence represents the protein encoded by the epsI gene from the Streptococcus thermophilus exopolysaccharide (EPS) synthesis operon. The operon has 13 open reading frames (ORF) designated epsA-M encoding proteins AAW22169-81. This protein has 24% identity to a protein
                                                                                                                                                                                                               Claim 7;
                                                                                                                                                                                                                                         DNA of lactic acid bacteria - e exo-polysaccharide biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S.thermophilus exopolysaccharide synthesis
                                                      Sequence
                                                                                                                                                                                                                                                                                      N-PSDB; AAT73236.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAAEVKIFLEIPK----EKEFEQAQKQLWHDIKKNRKAP 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDAYDYAYVQRPNSIMNSSFNLKKLDIIEMVHE-MENDIL-----AQFPNLALYVKNRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA----YELPEKDLPEEDFERARRFLYQCFKRTDTPP 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEAL-VKYRLHANQV-SSKHSVRQHEIAQGIQKTARNDFLQSMGFKTRFDSLE-YRQTKA
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                                                                                                                                                                                                               Page 14-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein; 324
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                                                        324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thermophilus.
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             11.9%;
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             Score 217.5; DB 18; Pred. No. 3.2e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168
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RESULT 13
AAY54072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                 22-APR-1998;
22-APR-1998;
22-APR-1998;
 of forming a bond (alpha or beta-isomer) between C-1 (carrying the reducing aldehyde function, of an activated D-galactose pyranose), and a phosphate on a lipophilic or proteinaceous primer. Stepwise synthesis of EPS occurs with, in each step, addition of a new sugar unit, through its hemi-acetyl function, to an alcoholic hydroxyl of a second sugar
                                                                               exopolysaccharides (EPS). These enzymes are designated EPS1-EPS10. and ere encoded by open reading frames eps1-eps10. The enzymes are isolated from Streptococcus thermophilus strain $fi39$. The proteins are used in a method for the synthesis of EPS, which includes at least one step
                                                                                                                                                                              Claim 3;
                                                                                                                                                                                                         New recombinant enzymes for synthesis particularly in lactic acid bacteria, fermented milk products
                                                                                                                                                                                                                                                                                                                       Stingele F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9962316-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Exopolysaccharide; RPS; ESS enzyme; EPS1; EPS2; EPS3; EPS4; EPS5; EPS6; EPS7; EPS8; EPS9; EPS10; Streptococcus thermophilus strain Sfi39; activated D-galactose pyranose; saccharide; beta-glycosyltransferase; transporter; food; fermented milk product; yoghurt; cheese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY54072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY54072 standard; Protein;
                                                                                                                                              AAY54065-74 represent enzymes involved in the biosynthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                    (NEST ) SOC
                                                                                                                                                                                                                                                                                                                                                                                                                                               22-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      flavour stability; organoleptic property.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63
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                                                                                                                                                                                                                                                                        2000-097267/08.
DB; AAZ45258, AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAAEVKIFLEIPK----EKEFEQAQKQLWHDIKKNRKAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KILAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA-----YELPEKDLPEEDFERARRFLYQCFKRTDTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VCSKFFLVDEKGSLLTKKEAPKKKSEVVSIEESIKILLLQQNGYDLA-----VWGKLY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVFSK-ENGGMSSARNFGIKK-AK-----GSFITFVDSDDYIVKDYLSHLVAGIKSETSI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDAYDYAYVQRPNSIMNSSFNLKKLDIIEMVHE-MENDIL-----AQFPNLALYVKNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEAL-VKYRLHANQV-SSKHSVRQHEIAQGIQKTARNDFLQSMGFKTRFDSLE-YRQTKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVSFFETISF - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTRHEDIAAFFPFGNPIHNNTMIMRRSVIDGGLRYDTERDWAEDYQFWYDVSKLGRLAYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IAMGAWL-----EVLSEE-----KDGNRLARHHKHGKIWKK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPS8
                                                                                                                                                                            Page 105-106; 162pp; French.
                                                                                                                                                                                                                                                                                                                                                    PROD NESTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               which is involved in exopolysaccharide biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                      Germond JE,
                                                                                                                                                                                                                                                                                                                                                                                 98EP-0201310.
98EP-0201311.
98EP-0201312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-EP02841
                                                                                                                                                                                                                                                                       AAY54072,
                                                                                                                                                                                                                                                                                                                                                      SA.
                                                                                                                                                                                                                                                                                                                      Lamothe
                                                                                                                                                                                                                                                                       AAY54073,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 AA
                                                                                                                                                                                                                                                                                                                      G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----PEGKLYEDMGTTYKLLKLASEVVF
                                                                                                                                                                                                                             for
                                                                                                                                                                                                                                           of exopolysaccharides,
                                                                                                                                                                                                                                                                        AAY54074.
                                                                                                                                                                                                                          improving properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290
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                                                                                                                                                                                                                           of.
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RESULT 14
AAY43774
DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                   22-APR-1998;
22-APR-1998;
22-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unit, present at the end of a chain of sugar residues bonded to the primer. EPS1 to EPS4 are used to elongate the EPS Chain, and to regulate EPS production, EPS5 creates new bonds between saccharides, EPS6 is used in the biosynthesis of EPS, EPS7 and EPS8 are beta-glycosyltransferases, EPS9 is a transporter of repetitive units, and EPS10 catalyses the conversion of a pyranose form of a beta-D-galactose to the furanose form. The EPS enzyme are used to improve properties of foods, particularly fermented milk products such as yoghurt and cheese,
                                                                                                                                                                                                                                                                                                                                                                                                  eps3; eps4; eps5; eps6; eps7; eps8; eps9; eps10; exopolysaccharide biosynthesis; EPS; intersugar bond; antitumour; probiotic; foodstuff; organoleptic quality; flavour; lactic acid bacteria; acidified milk product; yoghurt; cheese.
                                                  Claim 3; Page 106-107; 163pp; French.
                                                                                                         New recombinant enzymes
                                                                                                                                       N-PSDB;
                                                                                                                                                   WPI; 2000-013255/01.
                                                                                                                                                                                                                                                                                                                                               W09954475-A2
                                                                                                                                                                                                                                                                                                                                                                        Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                            eps operon; Streptococcus thermophilus Sfi39; enzyme; eps3; eps4; eps5; eps6; eps7; eps8; eps9; eps10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY43774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY43774 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g. their organoleptic properties and flavour stability.
                                                                                                                                                                                                        (NEST ) SOC
                                                                                                                                                                                                                                                                                          22-APR-1999;
                                                                                                                                                                                                                                                                                                                     28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 IVRGSF 119
                                                                                          .g. antitumor or probiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MNPLISIIVPTYNVEKYIRTCIESILAQTYRNIEVIIVNDGSTDQSLAVISDLICSHHNI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MQPLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IAMGAW 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVINQ-KNQGLSVARNTGID-----AATGKYIAFVDADDKIKPDFVSSLYQIADKTGAD 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KILAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
45; Conserv
                                                                                                                                      AAZ30355,
                                                                                                                                                                               Ή,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence of eps8 of Streptococcus thermophilus Sfi39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 AA;
                                                                                                                                                                                                         PROD NESTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                               Germond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                         thermophilus.
                                                                                                                                                                                                                                                98EP-0201310
98EP-0201311
                                                                                                                                                                                                                                     98EP-0201312
                                                                                                                                                                                                                                                                                         99WO-EP03011
                                                                                                                                    AAY43774, AAY43775, AAY43776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                              JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.8%;
35.7%;
                                                                                                            for
                                                                                                                                                                                                           SA
                                                                                                                                                                               Lamothe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29;
                                                                                            properties
                                                                                                         biosynthesis of exopolysaccharides having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 214.5;
Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                             or useful in fermented
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                             milk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
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AAY43767-76 represent the proteins encoded by the eps operon of Streptococcus thermophilus Sfi39. The operon contains 10 open reframes, and encodes enzymes (eps1, eps2, eps3, eps4, eps5, eps6

eps6,

reading

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RESULT 15
AAB47426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eps8, eps9 and eps10) that are involved in the biosynthesis of exopolysaccharides (EPS). The enzymes catalyse the formation of specific intersugar bonds. The enzymes catalyse a process that includes at least one step of forming a bond (in alpha or beta anomeric form) between Cl, carrying the reducing aldehyde group of an activated D-Galp (galactose in pyranose form), and a phosphate group on a lipophilic or proteinaceous primer. The enzymes are used to produce EPS that have antitumor or probictic properties or are used in foodstuffs to improve organoleptic qualities and flavour. When expressed by lactic acid bacteria. EPS impart a free-flowing character and/or a smooth, creamy texture to acidified milk products (yoghurt or cheese).
The sequences given in AAB47426-27 are encoded by a fragment of the plasmid derived from L. lactis subspecies cremoris Ropy352. The EPS plasmid is about 32 kb in size and encodes at least 13 active genes.
                                                                                                    Claim 28; Page 67-68; 73pp; English.
                                                                                                                                                        beauty cosmetics, comprises characteristics cremoris Ropy 352 -
                                                                                                                                                                             New bacterium useful in pharmaceutical formulations, food products and beauty cosmetics, comprises characteristics of Lactococcus lactis
                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                 Trempy JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-FEB-2000;
16-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157234-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               biosynthesis; fruit juice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPS plasmid; Lactococcus lactis subspecies cremoris Ropy352; exopolysaccharide; EPS352; milk; thickener; glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EpsN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB47426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB47426 standard; Protein; 332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-FEB-2001; 2001WO-US03404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 IVRGSF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVINQ-KNQGLSVARNTGID-----AATGKYIAFVDADDKIKPDFVSSLYQIADKTGAD 113
                                                                                                                                                                                                                                                                                    2001-488889/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KILAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IAMGAW 126
                                                                                                                                                                                                                                                                                                                                                                                      UNIV OREGON STATE.
US DEPT OF AGRICULTURE.
                                                                                                                                                                                                                                                               AAH43198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316
                                                                                                                                                                                                                                                                                                                                 Knoshaug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0179888
2000US-0241098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.8%; Score 214.5; DB 2
35.7%; Pred. No. 6.5e-14;
tive 29; Mismatches 45
                                                                                                                                                                                                                                                                                                                                    ΕP,
                                                                                                                                                                                                                                                                                                                                    Sandine WE,
                                                                                                                                                                                                                                                                                                                                 Ahlgren JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                 Dierksen KP;
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215 DSASK
                                           224 QVSSK 228
                                                                                                                                                                                                                    124 GAW------LE---VLSEEKD-GNRLARHHKHGKIWKKPTRHEDIAAFFP 163
                                                                                                                                                                                                                                                                   64 YNTKNLGVSHARNYGIDR-----ASGSYIMFLDPDDTYDKSYCLEMIGLINKFNADVVM 117
                                                                                                                                                                                                                                                                                                            64 AQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAM 123
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                                                                                                                               FGNPIHNNTMIMRRSVIDGGLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKYRLHAN 223
                                                                                                                                                                             SNYYICKGKNIYPNVNNDLLECEGLLSRDKTMRSILSDTGFKGFVW-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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219
                                                                                     --TRIFRKNVIN-NVKFNESINYLEDMLFNISIVHNARIIAYTNKRHYFYLQRE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Pred. No. 1.6e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                84;
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Search completed: December Job time: 38.1203 secs 2, 2002, 11:58:59

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Result
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(c) 1993 - 2002 Compugen Ltd
                                                        US-08-312-3878-3
US-08-683-426-3
US-08-683-428-3
US-08-878-360-3
US-08-683-428-11
US-08-683-428-11
US-08-683-428-11
US-08-478-14-08-8
US-09-333-412-11
US-08-478-14-08-8
US-09-333-412-11
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US-08-683-428-5
US-08-683-428-12
US-08-683-426-12
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US-09-134-001C-4051	PCT-US94-02552-9	US-08-967-506-9	US-08-967-508-9	PCT-US94-02552-19	US-08-967-506-19	US-08-967-508-19	US-09-134-001C-4067	US-08-961-083-202	US-09-134-001C-5633	US-08-961-083-168	US-08-858-207A-521	US-08-961-083-196	US-08-961-083-198	US-08-961-083-200	US-09-437-277-1	US-09-437-277-3	US-08-746-682A-10
Sequence 4051, Ap	Sequence 9, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 19, Appl		Sequence 19, Appl	Sequence 4067, Ap	Sequence 202, App	Sequence 5633, Ap	Sequence 168, App	Sequence 521, App	•	Sequence 198, App	Sequence 200, App	Sequence 1, Appli	Sequence 3, Appli	Sequence 10, Appl

ALIGNMENTS

RESULT 1 US-08-312-387B-3

Sequence 3, Application US/08312387B Patent No. 5545553
GENERAL INFORMATION:

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:

ADDRESSEE:

Klauber & Jackson

APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM

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TELEFAX: 20.1
TELEFAX: 3521
TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TVPE: amino acid
TVPE: amino acid
 Qy
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                                                                  QY
                                                                                                                                                                              US-08-312-387B-3
                                                                                                          Matches 348; Conserv
                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, VE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,3878
FILING DATE: July 7, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: Ju CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Hackensack
STATE: New Jerse
61 KILAQAQNSGLIPSLNIGLDELAKSGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSI 120
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Mismatches 0;
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US-08-683-426-3
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                                                                                                                                                                                                                                                                      NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
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MEDIUM TYPE: F10ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,426
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                                                                   al Similarity
348; Conserv
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                                                                 Score 1823; DB 1;
Pred. No. 5.5e-190;
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US-08-683-458-3
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                                                                                   Query Match
Best Local
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                                                                     Matches
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,458
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ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
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TOPOLOGY:
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CITY: F
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TELEPHONE: ZUI ...
TELEPHONE: ZOI 343-1684
                                                                y Match 100.0%;
Local Similarity 100.0%;
hes 348; Conservative (
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REFERENCE/DOCKET NUMBER: 600
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IVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
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                                                                Score 1823; DB 1;
Pred. No. 5.5e-190;
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US-08-878-360-3
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 Query Match
Best Local Similarity
Matches 348; Conserv
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APPLICANT: Gotsch
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                      TOPOLOGY: 1. MOLECULE TYPE:
                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acid
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TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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APPLICATION NUMBER:
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095B
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SOFTWARE: PatentIn Release #1.0, Version
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     Conservative
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SYSTEM: PC-DOS/MS-DOS
                                                                                                        linear
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                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                  September 26, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                100.0%;
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                Score 1823; DB 2;
Pred. No. 5.5e-190;
   Mismatches
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 Indels
                                  Length 348;
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RESULT 5
US-09-333-412-3
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Query Match
Best Local Similarity
Matches 348; Conserv
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                                                                                                                                                                                   TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 08/312,387
FILING DATE: JULY 1, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OLIGOSACCHARIDES, AND GENES ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                   LENGTH: 348 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/333,412 FILING DATE: 15-Jun-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New Jersey
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STREET: 411 Hackensack Avenue
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 Score 1823; DB 4;
Pred. No. 5.5e-190;
Mismatches 0;
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                                                                                                       US-08-312-387B-11
                                        Query Match
Best Local Similarity
Matches 347; Conserv
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                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
                                                                                                                                                                                                                   NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM NUMBER OF SEQUENCES: 12
                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08, FILING DATE: July 7, 1994 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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CITY: Hackensack
STATE: New Jerse
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                                                                                                                                TOPOLOGY:
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1 MQPLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRI 60
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                                              Conservative
                                                                                                                                  linear
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                                                                                                                 protein
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                                                           99.8%;
99.7%;
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                                            1;
                                         Score 1820; DB 1;
Pred. No. 1.2e-189;
1; Mismatches 0;
                                                                      Length 348;
                                            Indels
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                                           Gaps
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; MOLECULE TYPE: protein US-08-683-426-11
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Query Match
Best Local Similarity
Matches 347; Conserv
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Patent No. 5705367
GENERAL INFORMATION:
APPLICANT: GOTSCH
                                                                                                                                                                          TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                       NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095B
TELECOMMUNICATION INFORMATION:
                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/683,426 FILING DATE:
                                                                                                       TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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   Score 1820; DB 1;
Pred. No. 1.2e-189;
Pred. No. 1.2e-189;
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Query Match
Best Local Similarity
Matches 347; Conserv
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GENERAL INFORMATION:
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                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                    NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
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COUNTRY:
                                                                                                                                                                                         TELEPHONE: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Hackensack
                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                     LENGTH:
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        <u>ب</u>
                        Score 1820;
Pred. No. 1
     Mismatches
      1.2e-189;
hes 0;
                                       DB 1;
                                    Length 348;
        Indels
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US-08-878-360-11
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                                                                                                 TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                   FILING DATE:
APPLICATION NUMBER: 08/312,3
FILING DATE: September 26, 1
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
                                                                                                                                                NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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MEDIUM TYPE: Floppy
                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: '
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING T
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COUNTRY:
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CITY: H
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                     TELEPHONE: 201 %. TELEPHONE: 201 343-1684
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                                                                LENGTH:
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                                                                    348 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klauber & Jackson
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Query Match

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Score 1820;

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US-08-478-140B-3
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                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the America
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
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                                                                                                             TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ROTH, STEPHEN APPLICANT: ROTH, STEPHEN IE L.
APPLICANT: BUCZALA, STEPHEN IE L.
TITLE OF INVENTION: METHOD OF TRANSFERRING AT LEAST TWO
TITLE OF INVENTION: SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSFERASE,
TITLE OF INVENTION: POLYGLYCOSYLTRANSFERASE AND GENE ENCODING A
TITLE OF INVENTION: POLYGLYCOSYLTRANSFERASE
                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Laura A. COTUZZÍ
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 71:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: JOHNSON, KARL F.
                   MOLECULE TYPE:
                                                                                         SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
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                                                   TYPE: amino acid
                                     TOPOLOGY:
                                                                       LENGTH:
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                                                                     348 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1155 Avenue of the Americas
                                                                                                                                                 E: (212) 790-9090
(212) 869-9741/8864
                                     linear
                 protein
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1; Mismatches 0;
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RESULT 11
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                                                                                                           TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                 ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: No...
STATE: No...
COUNTRY: USA
TTD: 10036-2711
TTD: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BUCZALA, STEPHANIE L.

TITLE OF INVENTION: METHOD OF TRANSFERRING AT LEAST TWO
TITLE OF INVENTION: SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSF
TITLE OF INVENTION: POLYGLYCOSYLTRANSFERASE AND GENE ENCODING
TITLE OF INVENTION: POLYGLYCOSYLTRANSFERASE
                                                                                                                                                               NAME: LAURA A. COPUZZI
REGIZION NUMBER: 30,742
REFERENCEIDOCKET NUMBER: 718
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                         SEQUENCE CHARACTERISTICS
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/478,140B FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1155 A CITY: New York
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                                   TYPE: amino a
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                     TOPOLOGY:
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                                                    amino acid
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                                                                        348 amino acids
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99.7%;
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Pred. No. 1.
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RESULT 12
US-09-333-412-11
US-09-333-412-11
; Sequence 11, Application ...
; Patent No. 6342382
; Patent No. 6342382
; GENERAL INFORMATION: GOTSCHICH, English applicant: Gotschlich, English applicant: Gotschlich, English
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                                                                   INFORMATION FOR SEQ ID NO: 11:
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                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                              NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPHAX: 201 343-1684
TELEX: 133521
                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                             APPLICATION NUMBER: 08/312,387 FILING DATE: July 7, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS
OLIGOSACCHARIDES, AND GENES ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSGAWLDFAADGRMRRLFTLRQYFGILYRLIKNRRQARSDSAGKEQEI 348
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                                                                                                                                                                                                                                                             CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/333,412 FILING DATE: 15-Jun-1999
                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 411 Hackensack Avenue
                     LENGTH: 348 amino acids TYPE: amino acid
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99.7%;
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Pred. No. 1.2e-189;
1; Mismatches 0;
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US-09-338-943-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL
NAME: Laura A. COTUZZI
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7188-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: JOHNSON, APPLICANT: ROTH, STE APPLICANT: BUCZALA, ; TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Laura A. Coruzzi
                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
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99.7%;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/338,943
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                                                                                                         US 08/478,140
7188-017
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Pred. No. 1.2e-189;
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TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT:
                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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                                              ATTORNEY/AGENT INFORMATION:
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                NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 3
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STATE:
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REFERENCE/DOCKET NUMBER:
                                                                      FILING DATE:
                                                                                                                                          FILING DATE:
                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30
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WENTION: METHOD OF TRANSFERRING AT LEAST TWO
NVENTION: SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSF

WENTION: POLYGLYCOSYLTRANSFERASE AND GENE ENCODING

WENTION: POLYGLYCOSYLTRANSFERASE
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                30,742
                                                                                    08/478,140
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Pred. No. 1.2e-189;
1; Mismatches 0;
 7188-017
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-- rocal Similarity
-- ronser
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                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: GOLSChlich, Emil C.
APPLICANT: GOLSChlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERAN
TITLE OF INVENTION: OLIGOSACCHARIDES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION
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            NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600
                                                                              APPLICATION NUMBER: US/08 FILING DATE: July 7, 1994 CLASSIFICATION: 435
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                                                                                                                                                                                                                                         ZIP: 07601
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                                                                                                                                                                                                                                                                         STATE
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99.7%;
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GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
                                                                                                                   US/08/312,387B
                600-1-095
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Pred. No. 1.2e-189;
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; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR ESQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-312-387B-5
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Search completed: December Job time: 13.9535 secs
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1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

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Listing first 45 summaries
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           9
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12 US-10-007-267-1

12 US-10-007-267-1

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13 US-09-97-041-3

14 US-09-767-041-3

15 US-09-767-041-3

16 US-09-767-041-3

17 US-09-767-041-3

18 US-09-767-041-3

19 US-09-767-041-3
                                US-09-816-028A-27

US-09-767-041-35

US-09-816-028A-29

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ALIGNMENTS

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RESULT 1
US-10-007-267-3
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Patent No. US20020127682A1
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
            TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Jun-1999
APPLICATION NUMBER: 08/212,387
FILING DATE: July 7, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/007,267
FILING DATE: 03-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
TYPE: amino acid
                                                                                                                TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Klauber & Jackson
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RESULT 2
US-10-007-267-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/10007267 Patent No. US20020127682A1 GENERAL INFORMATION:
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                                                   REFERENCE/DOCKET NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Jun-1999
APPLICATION NUMBER: 08/312,387
FILING DATE: July 7, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: GOTSCHlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSPERASES FOR BIOSYNTHESIS
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                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/007,267 FILING DATE: 03-Dec-2001 CLASSIFICATION: <Unknown>
                 TELEFAX: 201 343-1684
TELEX: 133521
                                                                                                        NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New Jersey
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SEQ ID NO: 11:
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Pred. No. 1.9e-163;
Mismatches 0;
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Patent No. US20020127682A1
GENERAL INFORMATION:
GENERAL INFORMATION:
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APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Jun-1999
APPLICATION NUMBER: 08/312,387
FILING DATE: JULY 7, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
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                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                      APPLICATION NUMBER: US/10/007,267
FILING DATE: 03-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                STATE: New Jersey COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 411 Hackensack Avenue CITY: Hackensack
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FELEFAX:

201 343-1684

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TYPE: amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-007-267-5
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INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/007,267
FILING DATE: 03-Dec-2001
CLASSIFICATION: <Unknown>
                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAMGAWLEVLSEENNKSVLAAIARNGAIWDKPTRHEDIVAVFPFGNPIHNNTMIMRRSVI 178
                                                             R APPLICATION DATA:
APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Jun-1999
APPLICATION NUMBER: 08/312,387
FILING DATE: July 7, 1994
                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                            ZIP: 0760:
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
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                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/10007267
Jackson Esq., David A. FRATION NUMBER: 26,742
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APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
APPLICANT: Meyers, Rachel
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226, AND
TITLE OF INVENTION: 58764,
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE FAMILY MEMBERS AN
FILE REFERENCE: 38155-20034.00
CURRENT APPLICATION NUMBER: US/09/924,358
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/229,300
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
TYDE: DET
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                                                                               ; OTHER INFORMATION: US-09-924-358-29
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                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
                                                                                                                      FEATURE:
                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                            TYPE: PRT
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les 213; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KILAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEEIRAGYWKAAGIAVGADCLNYGLLKSTAYALYEKALSGQDIGCLRLFLYEYFLSLEKY 298
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TELEFAX: 201 343-1684
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Conservative
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64.28;
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                 Score 230; DB 10;
Pred. No. 1.5e-14;
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Mismatches
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                                      Length 150;
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; OTHER INFORMATION: CPS2K
US-09-767-041-22
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US-09-767-041-22
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Patent No. US20020055168A1
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SEQ ID NO 22
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CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: PCT/NL99/00460
PRIOR FILING DATE: 1999-07-19
PRIOR APPLICATION NUMBER: EP98202465.5
PRIOR FILING DATE: 1998-07-22
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PRIOR APPLICATION NUMBER: EP98202467.1
PRIOR FILING DATE: 1998-07-22
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TYPE: PRT
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                                     330 LIK-NRRQA 337
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285 QLKQNKRLA 293
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                                                                                                                                                                                                                                                                                                                     117 GYDRV-----
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les 87; Conserv
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                                                                                                                                                                                            ANQV--SSKHSVRQHEIAQGIQKTARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEKDLP 279
                                                                                                                                                                                                                                      LEADGHRFVVAWNKLYKKELFDFRFEKGKIHEDEYFTYRLLYELEKVAIVKECLYYYVDR 209
                                                                                                                                                                                                                                                                                                                                                                                               KKENGGLSDARNYGISR-AK-----GDYLAFIDSDDFIHSEFIQRLHEAIERENALVAVA 116
                                                                                                                                                                                                                                                                                                                                                                                                                      QAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAMG 124
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                                                                                                                EEDFERARRFLYQCFKRTDTPPSGAWLDFAA------DGRMRRLFTLRQYFGILYR 329
                                                                                                                                                       ENSIITSSMTDHRFHCLLE--FQNERMDFYESRG---
                                                                                                                                                                                                                                                                                                                                                      AWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNPIHNNTMIMR-RSVIDGG 183
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                                                                                                                                                                                                                                                                                                                   -----DASGHFLTAEPLPTNQAVLSGRNVCKKL 149
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                                                                            ---SFLAFAVLFLGKYNHWLSKQQKKLQTL---FRIVYK
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Pred. No. 6.1e-14;
68; Mismatches 99;
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US-09-900-038A-1
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Best Local Similarity
Thes 68; Conserve
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US-09-767-041-36
US-09-900-038A-1
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LENGTH: 278
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                                                                                     SOFTWARE: PatentIn Ver. SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09900038A Patent No. US20020142425A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                    APPLICANT: Miyake, Katsuhide APPLICANT: Watanabe, Masaki APPLICANT: Iijima, Shinji TITLE OF INVENTION: Beta 1,3-galactosyltransferase and DNA encoding the FILE REFERENCE: 766.53
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NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: PCT/NL99/0046(
PRIOR FILING DATE: 199-07-19
PRIOR APPLICATION NUMBER: EP98202465.5
PRIOR APPLICATION NUMBER: EP98202467.1
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TITLE OF INVENTION: STREP
FILE REFERENCE: 2183-4726
                                                                                                                              PRIOR APPLICATION NUMBER: JP 2001-392 PRIOR FILING DATE: 2001-01-05 NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/900,038A CURRENT FILING DATE: 2001-09-21
                                        LENGTH: 31
TYPE: PRT
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                    ORGANISM: Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 RENSITTS-SMTDHRFHCLLEFQNERMDFYESRGDK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 HANQVSSKHSVRQHEIAQGIQ-KTARNDFLQSMGFK 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 QAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAMG 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 VSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRIKILA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEADGHRFVVACNKLYKKELFEDFRFEKGKIHEDEYFTYRLLYELEKVAIVKECLYYYVD 212
                                                               313
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Pred. No. 6.6e-14;
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; OTHER INFORMATION: CPS1I
US-09-767-041-34
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US-09-767-041-34
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                                                                                                                                                                                                      Query Match
Best Local Similarity 23.1
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appr.ICANT: Smith, Hilda
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                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
SEQ ID NO 34
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT, PRIOR FILING DATE: 1999-07-19 PRIOR APPLICATION NUMBER: EP9
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Streptococcus suis FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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                                      121
 114
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                                                                                            KILAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSI 120
                                                                                                                                                                 MQPLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVLICAYNVE-KYFAQSLAAVVNQTWRNLDILIVDDGSTDGTL-AIAKDFQKRDSRIKIL 63
IAE---IDFCLVDENGYTKKKRNSNFHVL---TREETVKEFLS-GSNIENNVWCKLYSRD 166
                                IAMGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNPIHNNT--MIMRRS 178
                                                                                                                                                MNDLISVIVPIYNVQDYLDKCINSIINQTYTNLEVILVNDGSTDDSEKICLNYMKNDGRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -EIAQGIQK-----TARNDFLQSMGFKTRFDSLEYRQTKAAAAYELPEKDLPEEDFERA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SATLIELIDQK-GNLVYKQRESNKIYLT----NDIRKMLLNRSILAHPTWCVKKKVFDKL 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIIMSVYNEPLNYVRDSVESILNQTLTDFEFIIVIDNPSRGDLKQFLTEYSVVDNRIKIL 63
                                                                         KYYKKI-NGGLADARNFGLEHAT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn version 3.0
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27.8%; Pred. No. 2.7e-12;
tive 55; Mismatches 123;
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                                                                                                                                                                                                                     Mismatches
                                                                       -GKYIAFVDSDDYIEVAMFERMHDNITEYNAD 113
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                                                                                                                                                                                                                                                        Length 322;
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US-09-816-028A-27
Sequence 27, Application US/09816028A
Patent No. US20020042369A1
GENERAL INFORMATION:
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US-09-879-959-10
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US-09-879-959-10
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                                                                                                                                                                                                           RESULT 11
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SEQ ID NO 10
LENCTH: 972
TYPE: PRT
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APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis
TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
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PRIOR APPLICATION NUMBER: 09/469,200
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 09/178,851
PRIOR FILING DATE: 1998-10-26
NUMBER: 05/178,851
                                                                                       APPLICANT: Gilbert, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Weigel, Paul H
APPLICANT: Kumari, Kshama
APPLICANT: Kumari, Kshama
APPLICANT: Leangelis, Paul
TITLE OF INVENTION: STREPTOCOCCUS EQUISIMILIS HYALURONAN SYNTHASE GENE AND EXPRESS
TITLE OF INVENTION: IN BACILLUS SUBTILIS
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CURRENT APPLICATION NUMBER: US/09/879,959
CURRENT FILING DATE: 2001-09-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity les 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 PLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRIKI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                          V--YTTNRNVNPDGSLIA----NGYNWPEFSREKLTTAMI----AHHERMFTIRAWHLT
                                                                                                                                                                                                                                                                                                                        QKTARNDFL---QSMGFK-----TRFDSLE----YRQTKAAAYE 272
                                                                                                                                                                                                                                                                                                                                                                                                               DGGLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKYRLHANQVSSKHSVRQHEIAQGI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNPIHNNTMIMRRS--VI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSK-PNGGIASASNAAV-SFAK-----GYYIGQLDSDDYLEPDAVELCLKEFLKDKTLAC 552
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                                                                                                                                                                                                                                                                             QK--KNHFVVVNQSLNRQGITYYNYDEFDDLDESRKYIFNKTAEYQ
                                                                                                                                                                                                                                                                                                                                                                       DG---FNEKIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIK-----KLGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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FILE REFERENCE: 019633-000111US
CURRENT APPLICATION NUMBER: US/09/816,028A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: US 09/495,406
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 27
LENGTH: 301
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                                                                  US-09-767-041-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-767-041-35
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Best Local Similarity
                    Query Match
                                                                                                                                                                                                                        SOFTWARE:
SEQ ID NO 35
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                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: STREPTOCOCCUS SUIS VACCINES AND DIAGNOSTIC TESTS FILE REFERENCE: 2183-4726
CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22
                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998
                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/NL99/00460 PRIOR FILING DATE: 1999-07-19
                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: EP98202465.5 PRIOR FILING DATE: 1998-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                               ORGANISM: Streptococcus suis FEATURE:
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OTHER INFORMATION: OH4384 (ORF 6a of lipooligosaccharide (LOS)
                                                                                                                                                                               TYPE: PRT
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                                                                                      OTHER INFORMATION: CPS1J
                                                                                                        NAME/KEY: misc_feature
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                                                                                                                                                                                                  LENGTH: 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 NNSICNTKNEVLVKNNIQELQLVL -- NYLRQNYILNKYCSVLYVLIKYLLY 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 ANQV-SSKHSVRQHEIAQGIQKTARNDFLQSMGFKTRFDSLEYRQTKAAAY 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIHNNTMIMRRSVIDG----GLRYDTERDWAEDYQFWYD-VSKLGRLAYYPEALVKYRLH 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FFNAIVESNVISYKKFDFNSGFYSKKEFVKKIIAKKNLYWTMWGK--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith, Hilda
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10.7%;
24.7%;
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Pred. No. 7.3e-11;
6; Mismatches 100;
Score 194.5; DB Pred. No. 9e-11;
                    10;
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US-09-816-028A-29
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LENGTH: 303
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis.
TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
FILE REFERENCE: 01963-000011US
CURRENT APPLICATION NUMBER: US/09/816,028A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR APPLICATION NUMBER: US 09/495,406
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 2000-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 49 SOFTWARE: PatentIn Ver. ?
                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Campylobacter glycosyltransferase B (CgtB) beta-1,3 OTHER INFORMATION: galactosyltransferase from C. jejuni serotype 0:2 OTHER INFORMATION: (strain NCTC 11168)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Campylobacter jejuni FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 KNFMNLYINNIFSTPVCKLYKKRYITDLFQENQWLGEDLLFNLHYLKNIDRVSYLTEHLY 207
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                                          111 GGGKIDLLCFEAFITNAKKSIKKL--NIKQGKYNNKEFTMQILKTKNPFWTMWAKIIKKD 168
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172 TMIMRRSVIDGGLRYDTERDWAEDYQFWYDVSKL-GRLAYYPEALVKYRLHANQV-----
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                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                        65 QAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAMG 124
                                                                                                                                                                                                                4 ISVIVPVYNVDKYLSSCIESIINQNYKNIEILLIDDGSVDDSAKICKEYEK-DKRVKIFF
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                                                                                                                                NEENLKLLRARYEGA-KVATS-----PYIMFLDSDDYLELNACEECI------KILDMG 110
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                                                                                                                                                                                                                                                                                                       62;
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                                                                                  ----VLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPF----GNPIHNN 171
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                                                                                                                                                                                                                                                                                                     Score 194; DB 10;
Pred. No. 9.2e-11;
6; Mismatches 97;
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-765-272-200
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US-09-765-272-200
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                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                      Matches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
233 QHEIAQGIQKTARNDFLQSMGFKTRFDSLEYRQ------TKAAAYELPEKDL 278
                                        149
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                                                                                                                 111 FHILGD--
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                                                                                                                                               142 HHKHGKIWKKPTRHEDIAAFFPFGNPIHNNTMIMRRSVIDGGLRYDTER------DWA 193
                                                                                                                                                                                                                                                               ς,
                                                                                                                                                                                        61
                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: BYOOKES, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                    KLYKARLFEQLRFDIGKLGEDGYLNQKVYLLSEKVIYLNKSLYAYRIRKGSLSRVWTEKW 208
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                                                                        EDY-----QFWYDVSKLG-----
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                                                                                                                                                                                                                                                           LDSITTOTYKNIEIVVVNDGSTDASGEICKEFSEMDHRILYIEQ-ENAGLSAARNTGLNN 60
                                                                                                                                                                                    MS-----GNYVTFVDSDDWIEQDYVETLYKKIVEYQADIAVGNYYSF--NESEG--MFY 110
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STATE: Maryland
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21.2%; Pred. No. ...
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Search completed: December Job time: 8.97495 secs
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LENGTH: 270
TYPE: PRT
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Best Local (
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APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
FILE REFERENCE: 0.19633-00011115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-01-31 NUMBER OF SEQ ID NOS: 49
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PRIOR APPLICATION NUMBER: US 09/495,406
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                                                                             EENPNGRYENKNKEILNQNYHDKKKSNEIIKKLSKEFAHDEFHQKLFEVLKREEAGVKNR
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hypothetical prote
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45	44	43	42	4.1	40	39	38	37	36	35	34	ω ω	32	31	30
201.5	203	203.5	204	204.5	205	205	205.5	206.5	208.5	208.5	210.5	213	214	216	216.5
11.1	11.1	11.2	11.2	11.2	11.2	11.2	11.3	11.3	11.4	11.4	11.5	11.7	11.7	11.8	11.9
314	316	327	318	250	344	299	311	323	972	389	344	322	280	301	344
N	N	N	Н	2	2	ν	Ν	2	Ν	N	2	N	N	2	Ν
A71157	AE2189	AB1211	E71690	A64099	AC0974	в83557	T00087	AD2189	T09595	E81318	A70037	T44647	E71703	F95205	G70036
hypothetical prote	hypothetical prote	glycosyltransferas	minor teichoic aci	glycosyl transfera	probable glycosylt	probable glycosyl	rhamnosyltransfera	hypothetical prote	glucuronosyltransf	probable galactosy	capsular polysacch	glycosyl transfera	glycosyl transfera	glycosyl transfera	spore coat polysac

ALIGNMENTS

lactor N-neotetraose biosynthesis glycosyl transferase NMA0524 [imported] - Neisseria C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: H81970
C;Accession: H81970
C;Accession: H81970
N; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491
A;Accession: H81970
A;Status: preliminary
A;Residues: 1-346 <-PAR>
A;Residues: 1-346 <-PAR>
A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83816.1; PID:g737
A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83816.1; PID:g737
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: 1gth; NMA0524
C;Superfamily: Neisseria meningitidis glycosyl transferase A 밁 20 망 Ş Qy B Q 밁 Вþ Ωy Best Matches Query Match 299 301 239 241 179 181 119 121 61 61 Local 1 MQPLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRI 60 IAMGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNPIHNNTMIMRRSVI 180 PSGAWLDFAADGRWRRLFTLRQYFGILYRLIKNRRQARSDSAGKEQEI IAMGAWLEVLSEEKDGNRLARHHRHGKIWKKPTRHEDIADFFPFGNPIHNNTMIMRRSVI MQPLVSVLICAYNVEKYFAQSLATVVNQTWRNLEILIVDDGSTDGTLAIAKDFQKRDSRI 328; PAGAWLDFAADGKMRRLFTMRQYFGILHRLIKNRRQARSDSAGKEQEI Similarity Conservative 93.9%; Score 1712; DB 2; Length 94.3%; Pred. No. 1.6e-134; 10; Pred. No. 1.6e-134; 0; Mismatches 8; Indels 346 2; Gaps 300 240 60 238 178 1;

RESULT D81027

Gaps

1;

60

60

180

239 240

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CCA
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A; Note: the nucleoti
C; Genetics:
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A;Title: Molecular analysis of a locus for the biosynthesis ar A;Reference number: S70812; MUID:96414473; PMID:8817494
A;Accession: S70813
                                                                                                                                                                                                                                                                                                                                            glycosyl transferase A (EC 2.4.-.-) - Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: S70813
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C;Superfamily: Neisseria meningitidis glycosyl transferase
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A;Molecule type: DNA
A;Residues: 1-349 <TET>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Science 287, 1809-1815, 2000
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                                                                                                               A; Gene:
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A; Residues: 1-333 < JEN>
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                                                                                                                                                                                                                               A; Status: preliminary; nucleic acid
Query Match
                                                  Superfamily: Neisseria meningitidis Reywords: glycosyltransferase
                                                                                           Start codon:
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Best Local
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Pred. No. 5.2e-1
                Score 1617.5;
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                                                                       glycosyl
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                333;
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merty, B.
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C; Superfamily: Neis:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Science 269, 496-512, 1995
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A; Residues: 1-323 <TIGR>
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              SGAWLDFAADGRMRRLFTLRQYFGILYRLIK 332
                                                                                       KTARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEKDLPEEDFERARRFLYQCFKRTDTPP
                                                                                                                               HKLIFNKDYPYAEDYKFWSEVSRLGCLANYPEALVKYRLHGNQTSSVYNHEQNETAKKIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309;
                                                                                                                                                                                                                                                                                                                                                                                                                                              al Similarity
137; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB:U32832; GB:L42023; NID:g1574421; PIDN:AAC23227.1; seria meningitidis glycosyl transferase A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.5%;
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                                                  -----SVSLLEIYHVDKSNKVLKSILYEMYMSLDKYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 611.5; DB 1;
Pred. No. 3.8e-43;
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3; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                113;
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Gaps

5

PID:g1574422

64

62

181

177 241

influenzae

H.O.;

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A;Cross-references: GB:AL591985; PIDN:CAC49255.1; PID:g15140741; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymb
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fishe
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.;
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.;
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
C:Genetics:
                                                                            RESULT 6
B97168
(imported) - Clostridium acetobutylicum glycosyltransferase [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum 14-Sep-2001 #text_che C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_che C;Accession: B97168
C;Accession: B97168
C;Accession: B97168
C;Accession: B97168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable glycosyltransferase protein SMb21189 [imported] - Sinorhizobium meC;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
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A; Title: The complete sequence of the 1.683-kb psymB megaplasmid A; Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
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                                                                                                                                                                                                                                                                                                                                           Вb
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A;Genome: plasmi
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A; Residues: 1-367 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKYRLHANQVSSKH--SVRQHEIAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRIKI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITSLLHFIK--YHLELFDLKQNLKIIKKFIR 317
                                                                                                                                                                                                                                                              FYFLYQLIAEEEQPRLTHEFLTRTGKW-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGTGIDMLI----GNRIIR-GKPNPIY-RPGSLRILSMFFTI---FMHSTVVYNRNVIPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNPIHNNTMIMRRSVI-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISR-ENRGLIATINEGL-ALAK-----GELIARMDADDIAYPSRLSRQVALFSAEPRLAL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVVSIVLPVYNAEPYIAAAIESVLRQDYERLEVIAIDDGSTDRSRDILERYRKSDSRVSI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103;
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29.5%;
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Pred. No. 2e-19;
8; Mismatches 1
                                                                                                                                                                                                                                                                 -GLIRR----RERYGLL
                                                          Markarova, K.S.; Smith, D.R.
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    Sinorhizobium meliloti

                    Solvent-Producing
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                                                                              Q.; Gibson,
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; Fisher, R.F.
                      Bacterium
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C; Genetics:
A; Note: wblC
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A;Title: The genes responsible for O-antigen synthesis of A;Reference number: Z22749; MUID:99453293; PMID:10521656
A;Accession: T44330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: T44330 R;Yamasaki, S.; Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimada,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glycosyl transferase homolog [imported] - Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-333 < KUR>
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                                                                                                                                                                                                                                                                                                PLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRIKI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIQKTARNDFLQSMGFKTRFDSLEYRQTK 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRDNNMGMYYSLNEGIDR-AK-----GSYVARMDADDIALPERFERQIEYLNKNKDVDIL 114
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QLDYVYNENFRNSQDYELWSRIAEKTRFYTIQKPLLFYR--
                                     GLRYDTERDW--AEDYQFWYDVSKLGRLAYYPEALVKYRLHANQVSSKHSVRQHEIAQGI 240
                                                                                                                         MGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNPIHNNTMIMRRSVIDG
                                                                                                                                                                                                              LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALGGYNLNYKR--TEDYNLWLRAIAKGYKIAMLEEKLMKIRLH-----
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                                                                                                                                                                      ISRV-NKGLPYSLNEAI-SVSKA-----NYIARMDADDISLPERLETQLAVMENNPDIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --GGLRYDTERDWAEDYQFWY-DVSKLGRLAYYPEALVKYRLHANQVSSKHSVRQHEIAQ 238
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80; Conser
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29.7%;
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Pred. No. 1e
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Pred. No. 1.0
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1e-16;
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glycosyltransferase [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: H97167
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson,
Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 483-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bact
A;Accession: H97167
A;Accession: H97167
A;Status: preliminary
A;Residues: preliminary
A;Residues: 1-333 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK80131.1; PID:g15025167; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Accession: AG2188
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C; Ac
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A; Residues: 1-321 <KUR>
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30-Jun-2002
                                        GSPDB: GN00168
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R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gib: Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Datyriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing 1A;Reference number: A96900; MUID:21359325; PMID:21359325
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A;Molecule type: DNA
A;Residues: 1-336 <KUR>
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                                                                --LRGYRKEYDTAEDYDLWLRAIRNGYKIVRMDECLIKYRVH-NKSKTAVEMFNPKMVEY
                                                                                             GGLR-YDTERDWAEDYQFWYDVSKLG-RLAYYPEALVKYRLHANQVSSKHSVRQHEIAQG 239
                                                                                                                                                                                                                                                                                                                        LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122 ::: :: ||: ||| ||: :| :: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIDGGLRYDTERDWAEDYQFWYDVSKLGRLAY-YPEALVKYRLHANQVSSKHSVRQHEIA 237
                                                                                                                                                                                                                                MGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNPI-HNNTMIMRRSVID 181
                                                                                                                                                                                                                                                                                                                                                                                                       PLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRIKI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGIKIKLIDVFKRE--FKKDFKYIVWGASNGGKI---TKEVLDEFFEKS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R-ENKGIVYSLNEAI-RLAK-----GEYIARMDADDISAPKRIEKQISFLKSHRDIDILG
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           IQKTARNDFLQSMGFKTRFDSL
                                                                                                                                                                            LGTRIEAFGDIDEKQKTI----YNSAFSIKFDSQNIEQVFLTSCAIPHPSVMFKKDSIVK 173
                                                                                                                                                                                                                                                                                              ISR-EHRGLVDSLNEGIN-IAR-----GKYIARMDADDISINNRIEKQFEFLELNKDVDI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKFKTG
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75; Conser
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28.6%;
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27.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 271; DB 2; I
Pred. No. 7.8e-15;
4: Mismatches 105;
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Pred No 6.4e-15;
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguc Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AIZ091
                                                                                                                                                                                                                                                                                                                                                                                                                                                    glucosyltransferase [imported] - Nostoc sp. (strain PCC 7120) c;Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. c;Date: 14-bec-2001 #sequence_revision 14-bec-2001 #text_change C;Accession: A12091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07433.1; A;Experimental source: strain C-125 C;Genetics: A;Gene: BH3714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirz Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B84114
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                                                                                                                                                                                      A; Experimental source: strain PCC C; Genetics: A; Gene: all2288
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                                                                                                                                                                                                                               A;Cross-references: GB:BA000019; PIDN:BAB73987.1; A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-343 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-271 <STO>
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Best Local Similarity
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                                            TMK-AKIDYINDTNKKDKVDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIIKAG-SYDRNLRRRQDYDLWF
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                       LSVIIPVYNSESSVAETLRSVLAQTYRDLEIIIVDDGSTDKSIDICKQFQ--DERIRIIH
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                                                                                                                             Similarity
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31.5%; Pred. No. 7e-14;
                                                                                                                             13.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45;
                                                                                                                             Score 252.5;
Pred. No. 2.8
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                                                                                                          Mismatches
                                                                                                      5; DB 2;
2.8e-13;
nes 100;
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30-Jun-2002
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                 hypothetical protein alr3071 [imported] - Nostoc sp. (Speciles: Nostoc sp. strain PCC 7120 is a synonym of C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 C;Accession: AH2189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycosyltransferase BH3657 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-200
C;Accession: A84107
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A;Residues: 1-732 <STO>
A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07376.1;
A;Experimental source: strain C-125
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacters.
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                                                                                                                                                                                                                                                                                                                  RQHEIAQGIQKTARNDFLQSMGFKTRFDSLE--YRQTKAAAYELPEKD----LPEEDFER
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                                                                                                                                                                                                                                                                                                                                                                                                           RRSVIDGGLRYDTERDWAEDYQFWYDVSKL-GRLAYYPEALVKY---RLHANQVSSKHSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IAMGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNP----IHNNTMIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KILAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSI 120
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  Y.; Wolk, C.P.; Kuritz,
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#text_change
Sasamoto,
                                                                                                      (strain
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                                                                                                        PCC 7120)
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                                        30-Jun-2002
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Watanabe,
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A; Experimental s
C; Genetics:
A; Gene: alr2836
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-322 <KUS:
A; Cross-references: GB:BA000019; PIDN:BAB74535.1; PID:g17131930; GSPDB:GN00179
A; Cross-references: GB:BA000019; PIDN:BAB74535.1; PID:g17131930; GSPDB:GN00179
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ans A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AH2189
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A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Accession: AE2160
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A; Molecule type: DNA
A; Residues: 1-318 <KUR>
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Best Local S
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Best Local Similarity
Matches 70; Conserv
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                                     124 GAWLEVLSEEKDGN--RLARHHKHGKIWKKPTRHEDIAAF--
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                                                                                                                                                                                           64 AQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAM 123
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                                                                                                                                                                                                                                                                                                                       5 VSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKR-DSRIKIL 63 :||:| || :: :||:
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                                                                                                                FQA-NQGQGGAFNAGF-----AAATGEVVAFLDADDVWKPHKLQRIV-EVFQTSDVVGV 114
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28.5%; Pred. No. 1.6e-12;
ative 61; Mismatches 112;
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                                     FPFGNPIHNNT 172
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, M.; Yasuda, N
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative glycosyl transferase alr2836 (EC 2.-.-).
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the European Bioinformatics Institute
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Hypothetical protein; Transferase; Glycosyltransferase;
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                                                                                                                                                                                                                                                                                                                                         "Identification and characterization of hetA, a gene that acts in the process of morphological differentiation of heterocysts. J. Bacteriol. 172:3131-3137(1990).

-:- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                               Holland
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90264305; PubMed=2111805;
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-131 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the En European Bioinformatics Institute. There are no restroy non-profit institutions as long as its content
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                                                                                                                                                                 AP003591; BAB74535.1; AF031959; AAC32401.1;
 96;
                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            D., Wolk C.P.;
   Conservative
                                                                   AA;
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                                                                   36388 MW;
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Nostocales;
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                  Score 243; DB 1
Pred. No. 1e-12;
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                                                                753C2FB59327D968 CRC64;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Kuritz T., Sasamoto (
a A., Kawashima K., Kir
M., Matsuno A., Muraki
M., Takazawa M., Yamada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332
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                                 DB 1;
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   112;
                              Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muraki
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YA57_METJA
Q58457;
15-JUL-1998
30-MAY-2000
16-OCT-2001
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HSSP; P39621;
TIGR; MJ1057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
                                                                                                                Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Complete profequence 290 AA; 35099 MW; 3F6A1B221C420D74
                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The Theorem The Theorem 1997 of the Theorem 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCIENCE 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=JAL-1 / DSM 2661 / ATCC 43
MEDLINE=96337999; PubMed=8688087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Complete genome sequence of the methanogenic archaeon, Methanococcus
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(Rel.
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39, Last sequence update)
40, Last annotation update)
transferase MJ1057 (EC 2.-.-).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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Q57022; P96336;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                    Complete SEQUENCE
                                                                                                                                                                                 InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                        EMBL; U32768; AAC22526.1;
HSSP; P39621; 1QGQ.
TIGR; HI0868; -
                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 269:496-512(1995).
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-Rd / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemophilus influenzae
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Score 204.5; DB 1;
Pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        notation update)
HI0868 (EC 2.-.-).
                                                                                                                                                  A5D8220129782E98 CRC64;
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                                                              1.1e-09;
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P11290; P22999;
01-JUL-1989 (Rel. :
01-OCT-1994 (Rel. :
16-OCT-2001 (Rel. :
                                                                             PIR; A302bs; v.-..
PIR; B3276; B33276.
ECOGEne; EG11266; yibb.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Pfam; PF00535; Glycos_transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sofia H.J., Burland V., Daniels D.L., Plu "Analysis of the Escherichia coli genome. region from 76.0 to 81.5 minutes.";
                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
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"The primary structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=89174812; PubMed=2647748;
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STRAIN=K12 / MG16
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InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Exopolysaccharide synthesis; Transferase;
SEQUENCE 266 AA; 30748 MW; 163268A421
                                                                                                                                                                                                                                                                                 "Molecular analysis of the ams operon required for exopolysaccharide synthesis of Erwinia amylovora.";
Mol. Microbiol. 15:917-933(1995)
-i- EUNCTION: INVOLVED IN THE BIOSYNTHESIS OF AMYLOVORAN WHICH FUNCTIONS AS A VIRULENCE FACTOR.
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15-JUN-2002 (Rel. 41, Last annotation update)
Amylovoran biosynthesis glycosyl transferase amsE
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                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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01-NOV-1997 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                 Pfam; PF00535; Glycos_transf_2; 1.
Exopolysaccharide synthesis; Transferase; Glycos
SEQUENCE 301 AA; 34788 MW; 99D0EE3080E6EC06
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Amylovoran biosynthesis glycosyl transferase
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Q46632;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular analysis of the ams operon required synthesis of Erwinia amylovora.";
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           AONSGLIPSLNIGLDELAKSGGGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Microbiol. 15:917-933(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSGA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MFSVLISLYNKEKPENLEQCLESLHQQTLNADEIVLVYDGPVSESLKAVATRWANLLPLV
                                            SVVIPAYNASESIITTLDCLNEQSYKNFDVIIVDDKSADA----
                                                                        SYLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRIKILAQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDGGLRYDTERDWAEDYQFWYDVSKLGR-LAYYPEALVKYRLHANQVSS-----KHSV
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                                                                                                                      Similarity
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                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=7596293;
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                                                                                                                    9.0%;
21.8%;
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                                                                                                      Mismatches
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RESULT 8
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01-NOV-1995
15-JUN-2002
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Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Presecan E., Pujic P., Purnelle B., Ropoort G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo
Sorokin A., Taconi E., Takagi T., Takahashi H., Takemaru K.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Vashitt B. Washitt B. Washirt B. Washirt B. Washirt B. Washirt B.
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P46917;
                              subtilis.";
Nature 390:249-256(1997).
                                                                                                                                   "The complete
                                                                                                                                                                                         Winters P., Wipat A., Yoshida K., Yoshida K.
                                                                                                                                                                                                                                                              Tosato V., Uchiyam
Viari A., Wambutt
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(Rel. 41,
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                                                                                                                                              Wedler E., Wedler H., Weitzenegger T.,
Yamane K., Yasunoto K., Yata K.,
H.F., Zumstein E., Yoshikawa H., Danchin A.;
sequence of the Gram-positive bacterium Bacill
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Last annotation updat
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                                          BIOSYNTHESIS
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RESULT 9
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01-NOV-1995
15-JUN-2002
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InterPro; IPR001173; Glycos_transf_2.
Pfam; PP00535; Glycos_transf_2; 1.
Transferase; Glycosyltransferase; Complete proteome.
SEQUENCE 446 AA; 53148 MW; BB3698D9B6858C42 CRC64;
                                                                                                                                                                    Bacillus subtilis
                                                                                                                                                                                                Minor teichoic acids biosynthesis
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Kunst F.,
             MEDLINE=98044033; PubMed=9384377;
                           STRAIN=168
                                                                                               STRAIN=168;
                                                                                                                                                       Bacteria; Firmicutes;
                                                                                                                                                                                                                                                       P46918;
                                         SEQUENCE FROM N.A
                                                                      Submitted
                                                                                   Freymond
                                                                                                            SEQUENCE FROM N.A
                                                                                                                                      NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                        KEFMFHLLKENTEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIAQGIQKTA----RNDFLQSMGFKT----RFDSL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -RRHTLTSTVLFD-----ESIKFWEDA-----IFFNQLLLKEKRYGAVAEGKYFYRKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKILAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRS
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d (AUG-1994)
Ogasawara N.,
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(Rel.
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                                                                                   Karamata
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                                                                                                                                                       Bacillales; Bacillaceae; Bacillus
                                                                    the
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                                                                    EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is not removed.
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Pred. No. 5.2e-06;
                                                                                                                                                                                                                                                                     PRT;
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protein gga
Albertini A.M., Alloni
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Moszer I.,

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Ra Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Ra Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Ra Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Ra Presecan E., Pujic P., Purnelle B., Rapport G., Rey M., Reynolds S.,
Ra Presecan E., Pujic P., Purnelle B., Rapport G., Rey M., Reynolds S.,
Ra Presecan E., Pujic P., Purnelle B., Rosche B., Rose M., Sadaie Y.,
Ra Presecan E., Schleich S., Schroeter R., Scoffone F.,
Ra Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sakiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Na Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sakiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Na Sekiguchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Na Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Vassarotti A.,
Na Takeuchi M., Wedler E., Wedler H., Weitzenegger T.,
Na Viari A., Wambutt R., Wandmott H., Vamane K., Yasumoto K., Yata K.,
Noshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
"The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Best I
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InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Transferase; Glycosyltransferase; Complete proteome.
SEQUENCE 900 AA; 107154 MW; FA66495488C2C62F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S. Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T. Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Erritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N., Ghims S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U13979; AAA73513.1; -. EMBL; Z99122; CAB15585.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 390:249-256(1997).
-I- FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF GALACTOSAMINE-CONTAINING MINOR TEICHOIC ACIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
                                                   227
                                                                                                       174
                                                                                                                                                                                                              125
                                                                                                                                                                                                                                                                  124
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FNHSLITESKNLIDIIKNHEQKIPLFLQYMVMHDLKWKLLIKDISETPLDENEYSEFLTL
                                                                                                                                                        VIDGGLRYDTERDWAEDYQFW-YDVSKLGRLAYYPEALVKYRLH---
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                                                SKHS-----VRQHE--IAQGIQKTARNDFLQSMGFK---TRFDSLEYRQTKAA 269
                                                                                                       L--KNIRFDENCKIGEDAKLVNLIISQKKKYGLVKEAKYHYRVREDGSSAMQTAKANKNW 231
                                                                                                                                                                                                                                                               GAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNPIH-----NNTMIMRRS 178
                                                                                                                                                                                                                                                                                                                                                                      AQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAM 123
                                                                                                                                                                                                                                                                                                                                                                                                                          SVIMPIYNVELYLTEAIESIINQTIGFENIQLILVNDDSPDKSEIICKEYAQKYPNNIVY 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVLICAYNVEKYFAQSLAAVVNQT--WRNLDILIVDDGSTDGTLAIAKDFQKRDSRIKIL 63
                                                                                                                                                                                                              VAIPIFFAEGRTG----EHNLNNKF--SSTRILDVEK-----EPHHILTHCCSTFIKKDA 173
                                                                                                                                                                                                                                                                                                                      AKKQNGGYSSARNYGLKY-----AEGRYIQFLDPDDLYSEGTFENVLNFFDEHKNEIDI 124
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22.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 161;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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2.2e-05;
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Matches 74
                                                                                                                                                                                        CONFLICT
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Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Philips C.A., Spriggs T., Heblom E., Cotton M.D.,
Weidman J.F., Philips C.A., Spriggs T., Baudek D.M., Brandon R.C.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Genem C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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16-OCT-2001 (Re
                                                                                                                                                           SEQUENCE
                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                   InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
                                                                                                                                                                                                                                                                                    EMBL; U32842; TIGR; HI1695;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 269:496-512(1995).
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Rd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization influenzae.";
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16-OCT-2001 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                      Complete
                                                                                                                                                                                                                                   Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter J.C.;
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 63
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LAQAQNSGLIPSLNIGLDELAKSGGGGGEYTARTDADDIASPGWIEKIVGEMEKDRSIIA 122
                                SVLMSLYIKENPQFLRECFESLVAQTRQADEIVLVFDGVVTPDLEFVVTEFETK-LPLKL 62
                                                             SYLICAYNYE--KYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLA-IAKDFQKRDSRIKI 62
                                                                                                            Similarity
                                                                                                                                                                                                                     proteome.
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46
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267
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                                                                                             Conservative
                                                                                                                                                                                                                                     protein; Transferase; Glycosyltransferase;
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transferase HI1695 (EC 2.
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30770 MW;
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                                                                                             47;
                                                                                            Score 146; DB 1;
Pred. No. 7.2e-05;
7; Mismatches 129
                                                                                                                                                         V -> G (IN REF. 1).
D -> E (IN REF. 1).
F -> S (IN REF. 1).
; A2F1A0532737D8C3 CRC64;
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                 This
                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94067019; PubMeg=8248031,
Becker A., Kleickmann A., Keller M., Arnold W., Puehler A.;
"Identification and analysis of the Rhizobium meliloti exoAMONP genes"
"Identification and analysis of the Rhizobium meliloti exoAMONP genes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Succinoglycan biosynthesis protein exoo (EC EXOO OR RB1084 OR SMB20959.
Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti.",

Proc. Natl. Acad. Sci. U.S.A. 98:9899-9994(2001).

-!- FUNCTION: GLYCOSYLTRANSFERASE REQUIRED FOR THE SYNTHESIS OF SUCCINOGLYCAN (EPS 1). NEEDED FOR THE ADDITION OF THE FIFTH SUGAR (GLUCOSE), CATALYZES THE FORMATION OF A BETA-1,6 LINKAGE BETWEEN (GLUCOSE), CATALYZES THE FORMATION OF A BETA-1,6 LINKAGE BETWEEN
                                                                                                                                                                                                                           MEDLINE=21396508; PubMed=11481431;
Finan T.M., Weidner S., Wong K., Buhrmester J.,
Vorhoelter F.J., Hernandez-Lucas I., Becker A.,
Golding B., Puehler A.;
                                                                                                                                                                                                                                                                                                                                involved in exopolysaccharide biosynthesis located on the exoHKLAMONP fragment."; mol. Gen. Genet. 241:367-379(1993).
                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=RCR2011 / SU47;
MEDLINE=94067019; Pubm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Bacteria; Proteobacteria; alpha subdivision;
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01-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           izobiaceae;
                                                                         PATHWAY: Exopolysaccharide biosynthesis.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY
                                                                                                                  THE FOURTH AND FIFTH SUGAR.
                                          CAUTION: Ref.1 sequence differs from that shown frameshift in position 208.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLRYDTERDWAEDYQFWYDVSKLG-RLAYYPEALVKYRLHANQVSSKHSVRQH------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGYE----DLQEDYYLWIKLYAQGLYMANLPDILVYARVGNGMVSRRRGVNQAKAEWRLF
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RESULT 12
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Best Local (
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                      MEDLINE-95020537; PubMed-7934828; Glaser P., Kunst F., Arnaud M., Coudart M. Hullo M.F., Tonescu M., Lubochinsky B., Ma Presecan E., Santana M., Schneider E., Sch Rapoport G., Danchin A.; "Bacillus subtilis genome project: cloning kb region from 325 degrees to 333 degrees. Mol. Microbiol. 10:371-384(1993).
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01-FEB-1995 (Rel. 3
15-JUN-2002 (Rel. 4
Putative 91ycosyl t
YWDF OR IPA-56D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00535; Glycos_transf_2; 1. Transferase; Exopolysaccharide
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
                                                                                                                                       STRAIN-168
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                               Bacteria; Firmicutes;
                                                                                                                                                                                                          Bacillus subtilis
                                                                                                                                                                                                                                                                                              P39614;
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SEQUENCE FROM N.A.
                                                                                                                                                                              NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                              YWDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRIKI 62
                                                                                                                                                                                                                                                                                                           BACSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VDN-LDVVS--LDGRSL-RMFSEAELARLP--QLTLPAFIESNVLFRSEHNFGYMKPIFE 175
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transferase ywdf (EC 2.-.
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Pred. No. 0.000
51; Mismatches
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                                                                                            Coudart M.P., Gonz
nsky B., Marcelino
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degrees.";
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C 2.-.-.).
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                                                   sequencing of the 97
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RA Azevedo V. Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Bridnell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Bridnell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Benizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Galleron N.,
RA Ghim S.Y., Glaser P., Koningstein G., Krogh S., Kumano M.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Median N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Perescott A.M.,
RA Parro V., Pohl T.M., Schleich S., Schroeter R., Scoffene F.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
The complete genome sequence of the Gram-positive bacterium Bacillus
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InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
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EMBL; Z99123; CAB15824.1;
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-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
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European Bioinformatics Institute. There a
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RRFLHDEIGYFDADVHNYW--DWDFYLRAAKDYRVKRVPCASVIYAFSDAGDNQSADLGA 213
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RESULT 13
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursler L., Brans A., Braun M., Brighell S.C., Bron S.,
RA Borvillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
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RA Rilbert H., Holsappel S., Holsono S., Hullo M.F., Itaya M., Jones L.,
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RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
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RA Ridger M., Fivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Schiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Schiguchi J., Tanaka T., Taraka T., Takemaru K.,
RA Yoshi A., Wallaco H., Tanaka T., Taraka H., Takemaru K.,
RA Yosh
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                                                                     Bacillus subtilis, in native and nucleotide-complexed forms."; Biochemistry 38:6380-6385(1999).
-!- FUNCTION: GLYCOSYLTRANSFERASE IMPLICATED IN THE SYNTHESIS OF THE
                                                                                                                                                                                                                                                                                                                                                                                          "The complete subtilis.";
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STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMed G. III, Bloch C.A., Pern Blattner F.R., Plunkett G. III, Bloch C.A., Pern Riley M., Collado-Vides J., Glasner J.D., Rode C Gregor J., Davis N.W., Kirkpatrick H.A., Goeden Mau B., Shao Y.;
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PDB; 1QGS; 04-MAY-00.
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                                        complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRIKI 62
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Pred. No. 0.00012;
6; Mismatches 87
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"A 718-kb DNA sequence of the Escherichia coli K-12 corresponding to the 12.7-28.0 min region on the lin DNA Res. 3:137-155(1996).

-i- SUBCELLULAR LOCATION: Integral membrane protein corresponding to Y.PESTIS HMS LOCUS PROTEIN HMSR A
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Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Oshima T., Aiba H., Baba T., Fujita K., Kashimoto K.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
SEQUENCE FROM N.A. STRAIN=ATCC 29342 MEDLINE=97105885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000204; AAC74107.1; EMBL; D90739; BAA35803.1; - EcoGene; EG13863; ycdQ.
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                                                                    Mycoplasma pneumoniae. Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB000010; AAB95728.1; -.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
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Nucleic Acids Res. 24:4420-4449(1996).
-i- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
STRONG, TO M.GENITALIUM MG060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome. SEQUENCE 299 AA; 35079 MW; 6E3F89EDAE420417 CRC64;
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                                                                                   205 HFKR 208
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O9Clr9 pasteurella
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Q9rgn2 neisseria g
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Q9rg44 streptococc Q9uzi6 pyrococcus Q9s410 leptospira	4		anabaena	Q8yzcl anabaena sp	Q8yw50 anabaena sp	anabaena	anabaena		anabaena	5 bacillus	Ωı		clostric	Q56869 yersinia en	Q8ysm2 anabaena sp		8	Q93ek8 neisseria m	=	2 rhizobium	Q9k2r3 neisseria g	\vdash	P96946 neisseria m

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Best Local :
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Q1-NOV-1996 (TrEMBLrel. 01,
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                       "Genetic locus for the biosynthesis of the variable portion Neisseria gonorrhoeae lipooligosaccharide.";
J. Exp. Med. 180:2181-2190(1994).
EMBL; U14554; AAA68009.1; -.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
                                                                                                                                                                                                                                                                                                                                                              Glycosyl transferase. LGTA.
                                                                                                                                                                   Transferase.
SEQUENCE 348 AA;
                                                                                                                                                                                                                                                                                                                                       Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
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                                                                    IAMGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNPIHNNTMIMRRSVI 180
                                  KILAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSI 120
                       KILAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSI
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Pred. No. 1.5e-148;
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Q9RGN2;
Q1-MAY-2000 (TrEMBLrel. 13, C
Q1-MAY-2000 (TrEMBLrel. 13, I
Q1-DEC-2001 (TrEMBLrel. 19, I
Glycosyltransferase.
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Harvey H.A., Porat N., Campbell C.A., Jennings M.,
Phillips N.J., Apicella M.A., Balke M.S.;
"Gonococcal lipooligosaccharide is a ligand for the
receptor on human sperm.";
Mol. Microbiol. 36:1059-1070(2000).
EMBL; AFI21135; AAF14359.1;
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
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SEQUENCE 346 AA;
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Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
CCBI_TaxID=485;
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Query Match
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Q93PS0;
Q1-DEC-2001 (TremBirel. 19, Cr. Ol-DEC-2001 (TremBirel. 20, L. Ol-MAR-2002 (TremBirel
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Q50951;
01-NOV-1996 (TIEMBLIEL C
01-NOV-1996 (TIEMBLIEL C
01-JUN-2001 (TIEMBLIEL 1
                                                                                                                   Neisseria gonorrhoeae.
Bacteria; Proteobacter
NCBI_TaxID=485;
gonorrhoeae
                     STRAIN=PID2;
Tong Y., Arking D.,
"Characterization o
                                                                                                                                                                                        Glycosyl transferase LGTA.
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SEQUENCE 362 AA;
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Interpro; IPR001173; Glycos_transf_2
Pfam; PF00535; Glycos_transf_2; 1.
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EMBL; U15992; AAA92074.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Danaher R.J., Levin J.C.,
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al Similarity 98.38;
342; Conservative
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PID2.";
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01-0CT-2000
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SEQUENCE
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Nature 404:502-506(2000).
EMBL; AL162753; CAB83816.1;
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
                                                                                                                                                                                     Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T. Bavies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Ho Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; "Complete DNA sequence of a serogroup A strain of Neisseria"
                                                                                                                                                                                                                                                                                                                                                                                         01-OCT 2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Lacto-N-neotetraose biosynthesis glycosyl tranferase.
                                                                                                                                                                                                                                                                                     STRAIN=Z2491 / SEROGROUP
MEDLINE=20222556; PubMed
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Bacteria; Proteobacteria;
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Pred. No. 3e-1
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EMBL; AF208058; AAF25876.1; -.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
SEQUENCE 322 AA; 37109 MW; 88FECA
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Bacteria; Proteobacteria;
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Pred. No. 2.36
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ
EMBL; AF208059; AAF25877.1;
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
SEQUENCE 321 AA; 37052 MW; 6ACADA9A3CB738
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Q9L8E9;
01-OCT-2000
SEQUENCE FROM N.A.
STRAIN=MC58 / SEROGROUP B;
MEDLINE=20175755; PubMed=10710307;
MEDLINE=20175755; Selbmed=10710307;
MEDLINE=20175755; PubMed=10710307;
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01-OCT-2000
                                                                                                                                                                                                                              Neisseria meningitidis
Bacteria; Proteobacteri
                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Lacto-N-neotetraose biosynthesis glycosyl transferase
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Bacteria; Proteobacteria;
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Pred. No. 8.4e-134;
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                     K.E.,
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Q51115,
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
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                           MEDIINE=96414473; PubMed=8817494;
Jennings M.P., Hood D., Peak I.R.A., Virji M., Moxon E.R.;
Jennings M.P., Hood D., Peak I.R.A., Virji M., Moxon E.R.;
"Molecular analysis of a locus for the biosynthesis and phase-variable expression of the lactor.N-neotetraose terminal lipopolysaccharide structure in Neisseria meningitidis.";
Mol. Microbiol. 18:729-740(1995).
EMBL; U25839; AAC44084.1; -.
EMBL; U25839; AAC44084.1; -.
Pfam; PF00535; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
SEQUENCE 333 AA; 38563 MW; 49D8F6CE375387BF CRC64;
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EMBL; AE002541; AAF42258.1;
TIGR; NMB1929; -
                                                                                                                                                                               STRAIN-MC58
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        Neisseria meningitidis.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                  Glycosyl tranferase
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Arking D., Tong Y., Stein D.C.;
"Analysis of lipooligosaccharide biosynthesis
J. Bacteriol. 183:934-941(2001).
EMBL; AF240672; AAG09764.1; -.
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Pfam; PF00535; Glycos_transf_2; 1.
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EMBL; AF355193; AAL12840.1; -.
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                                       Gotschlich E.C.;
"Genetic locus for the biosynthesis of the variable
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Bacteria; Proteobacteria;
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01-NOV-1996 (TrEMBLrel.
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Bacteria: Proteobacteria;
BCBI_TaxID=487;
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Neisseria gonorrhoeae lipooligosaccharide.";
J. Exp. Med. 180:2181-2190(1994).
                                                                                 MEDLINE=95053752; PubMed=7964493;
                                                                                                                             SEQUENCE FROM
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Q1-JUN-2001
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EMBL; AE006155; AAK03224.1; -...
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2.
Hypothetical protein; Complete proteome.
SEQUENCE 337 AA; 39267 MW; 8639BCFB5F700DB4 CRC64;
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Pred. No. 4.5e-49;
59; Mismatches 113
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EMBL; AB012956; BAA33603.1; -.
EMBL; U72485; AAC44837.1; -.
HSSP; P39621; 1060.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
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                                                                                                                                                                                                                                                                          Transferase.
SEQUENCE 337 AA;
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                                                                                                                                                                                                                                                                                                                                                                    "Cloning and sequence of a region of Vibrio its use in PCR-based detection.";
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97094999; PubMed=8940420; Falklind S., Stark M., Albert M.J., Uhlen M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamasaki S., Shimizu T.,
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            QGIQ
                                   YKINYDLGYKDAEDYKFWVDFSKYTLFSNVPEILLRYRYHQESISRVADNKENKERFEII
                                                                                                       MGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNPIHNNTMIMRRSVIDG
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                                                        -GLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKYRLHANQVS----SKHSVRQHEIA
                                                                                  CGTWVEVFGE-
                                                                                                                                 LVSRENKGLIVSLNEGLD-LAK-----GQYIARMDADDISIKSRFEKQIEFLDSNPDIGV
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            KTARNDFLQSMGFK----
-: -:
                                                                                  -NIKSKKWKMPTQDPDLKAKLTFSVPFAHPTVMIRKKVIDK
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Last annotation update)
glycosyltransferase A).
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Pred. No. 3.2e-27;
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RESULT 15
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ID 03423
AC 03423
AC 01-JA
DT 01-JA
DT 01-JU
DE Sugar
OS Vibri
OC Bacte
OC NCBI
RN [1]
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RC STRAI
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Search completed: December Job time: 31.8926 secs
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O34234;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Sugar transferase.
Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-AI-1837;
MEDLINE-97252505; PubMed-9098074;
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EMBL; Y07786; CAA69119.1; -.
HSSP; P39621; 1060;
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
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SEQUENCE 337 AA;
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Novel Vibrio cholerae O139 genes involved
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                                                                     SKIQ----NEVLTSVG
                                                                                                                                           YKINYDLGYKDAEDYKFWVDFSKYTLFSNVPEILLRYRYHQESISRVADNKENKERFEII 226
                                                                                                                                                               -GLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKYRLHANQVS----SKHSVRQHEIA 237
                                                                                                                                                                                                             CGTWVEVFGE-----NIKSKKWKMPTQDPDLKAKLTFSVPFAHPTVMIRKKVIDK 166
                                                                                                                                                                                                                                                                                LVSRENKGLIVSLNEGLD-LAK-----GQYIARMDADDISIKSRFEKQIEFLDSNPDIGV 116
                                                                                                                                                                                                                                                                                                      LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
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                  2, 2002, 12:02:15
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Copyright

GenCore version (c) 1993 - 2002

5.1.3 Compugen Ltd

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Minimum DB
Maximum DB
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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AAB44538
AAU99917
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AAY81561
AAW89327
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                Virulence gene pro
Virulence gene pro
Human 67210 glycos
Partial GLUT. Hae
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Lipo-oligosacchari
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9.4	9.4	9.4	•	•	•	•		9.5	•	•		10.0	•			•	•	•	•	10.7	•	11.1	11.1	11.1	•		•	•	•	•	11.9			11.9
365	345	282	390	390	384	372	372	361	305	341	365	364	323	351	361	357	357	413	674	674	401	441	409	392	272	361	346	346	332	312	398	313	346	332
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AAG13968	1396	AAG13970	ABB91529	AAG30295	AAG30296	AAB60318	AAW98360	AAG30297	AAG55049	ABB92615	AAG10401	AAG10402	AAG10403	ABB92218	AAG13327	ABB92767	AAG13328	ABP27412	ABP54656	AAW61238	ABP27413	AAG28025	AAG28026	AAG28027	ABP27661	ABB90816	ABB92808	AAG45490	AAG45491	ABP27411	ABP28550	9128	AAG15766	76
	Arabidopsis thalia	Arabidopsis thalia	11y	is	is	licobacter	GHI	_	is t	•	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia		- 1	٣	abidopsis	Streptococcus poly	S. pneumoniae SP11	Streptococcus pneu	Streptococcus poly	Arabidopsis thalia		Arabidopsis thalia	C 1	Ly	Herbicidally activ	is t	idopsis t	ptococcus	tococ	treptoco	is tha	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AAR91313
ID AAR9

AAR91313 standard; Protein; 306 AA

09-JUL-1996 AAR91313;

(first entry)

Glycosyltransferase; lipo-oligosaccharide; N. gonorrhoeae glycosyltransferase LgtC

lgt gene; LOS locus;

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Nucleic acids encoding diagnosis of infection oligo:saccharide(s)
                             WPI; 1996-200924/20.
N-PSDB; AAT14061.
                                                     Gotschlich
                                                                                                                 04-APR-1996
                                                                                                                                              Neisseria gonorrhoeae strain F62
                                                                                   26-SEP-1994;
                                                                                                  25-SEP-1995;
                                                                                                                                WO9610086-A1
                                                                   (UYRQ ) UNIV ROCKEFELLER.
                                                     EC;
                                                                                  94US-0312387
                                                                                                  95WO-US12317.
       glycosyl transferase(s) - used in the with Neisseria and for the biosynthesis
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Streptococcus

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RESULT 2
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Best Local S
Matches 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IgtC (AAR91313) can be obtd. by expression of the ligtC coding sequence in recombinant host cells. A method for adding Gal alphal-4 to Gal comprises contacting a reaction mixture contg. activated Gal to an acceptor moiety comprising a Gal residue in the presence of LigtC. Oligosaccharides can be produced that, when attached to non-toxic lipids, are useful for Neisseria vaccine prepn. Blood group core oligosaccharides, and mimics of lacto-N-neotetraose, gangliosides and saccharide portions of globoglycolipids can also be
           Buczala
                                                                                                                                                                     Neisseria
                                                                                                                                                                                                N-acetylgalactosaminyl transferase;
                                                                07-JUN-1995;
                                                                                         03-JUN-1996;
                                                                                                                  19-DEC-1996
                                                                                                                                                                                                           Polyglycosyltransferase; N-acetylglucosaminyl transferase;
                                                                                                                                                                                                                                     Lipo-oligosaccharide gene-encoded protein
                                                                                                                                                                                                                                                                 21-MAR-1997
                                                                                                                                                                                                                                                                                                                      AAW06578 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                     (NEOS-) NEOSE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 Glycosyltransferases (AAR91311-15) are products of the lgt locus (AAT14061) of Neiserria gonorrhoeae strain F62. Glycosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDIVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHYLDAGISEENRAAVAANLRGGGNIRF
                                                                                                                                                                                                                                                                                                                                                                                                                FLRKIY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSHYCGSAKPWHRDCTVWGAERFTELAGSLTTVPEEWRGKLAVPPTKCMLQRWRKKLSAR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNWVGACIDLFVERQEGYKQKIGMADGEYYFNAGVLLINLKKWRRHDIFKMSCEWVEQYK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDVNPEDFAGFPLNIRHISITTYARLKLGEYIADCDKVLYLDTDVLVRDGLKPLWDTDLG 120
                                                                                                                                                                                                                                                                                                                                                                                         FLRKIY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                         VSHYCGSAKPWHRDCTVWGAERFTELAGSLTTVPEEWRGKLAVPPTKCMLQRWRKKLSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVMQYQDQDTLNGLFKGGVCYANSRFNFMPTNYAFMANGFASRHTDPLYLDRTNTAMPVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVMQYQDQDILNGLEKGGVCYANSRENEMPTNYAFMANGFASRHTDDLYLDRTNTAMPVA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNWVGACIDLFVERQEGYKQKIGMADGEYYFNAGVLLINLKKWRRHDIFKMSCEWVEQYK
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           SL,
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                                                                                                                                                                     gonorrhoeae
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                                                                                                                                                                                                                                                                 (first entry)
         Johnson KF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2d; 81pp;
                                                              95US-0478140.
                                                                                       96WO-US08323
                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                      ATCC 33084
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           Roth S;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transfer of at least 2 saccharide units using poly:glycosyl:transferase - isolated from N. gonorrhoeae, catalyses the addition of both GlcNac and GalNac di:saccharide(s) units to a
                                                                                                                                                    Neisseria gonorrheae
                                                                                                                                                                                                                                 08-MAY-2001
                                                                                                                                                                                                                                                           AAB72456;
                                                                                                                                                                                                                                                                                    AAB72456 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stated in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2C-E; 38pp; English.
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N-PSDB; AAT49230.
                                                                          27-JUL-2000;
                                                                                                                                                                            UGGT; UDP-glucose:glycoprotein glucosyltransferase; enzyme; GLYT
                                                                                                                                                                                                       Partial GLYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single galactose moiety
                      (CANA ) NAT RES COUNCIL CANADA
                                                 18-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                  FLRKIY 306
                                                                                                                                                                                                                                                                                                                                                                            FLRKIY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVMQYQDQDILNGLEKGGVCYANSRENEMPTNYAEMANGFASRHTDPLYLDRTNTAMPVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNWVGACIDLFVERQEGYKQKIGMADGEYYFNAGVLLINLKKWRRHDIFKMSCEWVEQYK
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                                                                                                                                                                                                                                (first entry)
                                                                          2000WO-CA00883
                                                99US-0376330
                                                                                                                                                                                                                                                                                   Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1657; DB 18;
Pred. No. 4.8e-169;
); Mismatches 0;
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Bergeron JJM,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virulence gene; antibacterial; vaccine; septicemia; bronchopneumonia; rhinitis;
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                                               Attenuated Pasteurellaceae bacteria comprising mutations in virulence genes, useful as a live attenuated vaccine against bacterial infections
                                                                                                                                                                       WPI; 2000-647422/62
                                                                                                                                                                                                                                                                                                                                                                      09-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virulence gene protein #46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-FEB-2001
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                                                                                                                                                                                                                            Lowery DE, Fuller TE,
                                                                                                                                                                                                                                                                                 (PHAA ) PHARMACIA & UPJOHN INC
                                                                                                                                                                                                                                                                                                                                            10-SEP-1999;
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99US-0153453.
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RESULT 5
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    wide variety of animals. The present invention relates to virulence genes from Pasteurellaceae. The present sequence is a protein encoded by one such virulence gene. The virulence genes of the present invention may be mutated in order to produce an inactive gene. The inactive virulence gene may in turn be used to produce a vaccine, which is useful for treating bacterial infections such as septicemias, bronchopneumonias, rhinitis and
WPI; 2000-647422/62
N-PSDB; AAC79598.
                                                                                                   09-APR-1999;
10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                              AAB44538 standard; Protein; 302 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 39; Pages
                                          Lowery DE,
                                                                                                                                            06-APR-2000;
                                                                                                                                                                          19-OCT-2000
                                                                                                                                                                                                     WO200061724-A2
                                                                                                                                                                                                                                    Pasteurella multocida
                                                                                                                                                                                                                                                               septicemia;
                                                                                                                                                                                                                                                                           Virulence gene; antibacterial;
                                                                                                                                                                                                                                                                                                        Virulence gene protein #18
                                                                                                                                                                                                                                                                                                                                   08-FEB-2001 (first entry)
                                                                       (PHAA ) PHARMACIA & UPJOHN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDIVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEENRAAVAANLRG-GGNIR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family Pasteurellaceae encompasses several pathogens that infect a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLSARFLRKIY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYPNQMIYQDQDILNILFRNKVCYLDCRFNFMPNQLERIKQYHKGKLSNLHSLEK--TTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QYKDVMQYQDQDILNGLFKGGVCYANSRFNFMPTNYAFMANGFASRHTDPLYLDRTNTAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VNNFLTAACYDSFIENEKSEHKKSISMSDKEYYFNAGVMLFNLDEWRKMDVFSRALDLLA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGGNWVGACIDLEVERQEG-YKQKIGMADGEYYFNAGVLLINLKKWRRHDIFKMSCEWVE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MNILFVSDDVYAKHLVVAIKSI-INHNEKGISFYIFDLGIKDENKRNINDIVSSYGSEVN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIRYKFKYQVY 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVVISHYCGPEKAWHADCKHENVYFYQKILAEIT-----RGTDKERVLSIKTYLKALIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVAVSHYCGSAKPWHRDCTVWGAERFTELAGSLTTVPEEWRG--KLAVPPTKCMLQRWRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIAVNEKEFESFPVQISYISLATYARLKAAEYLPDNLNKIIYLDVDVLVFNSLEMLWNVD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIDVNPEDFAGFPLNIRHISITTYARLKLGEYIAD-CDKVLYLDTDVLVRDGLKPLWDTD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 AA;
                                          Fuller TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                             bronchopneumonia;
                                                                                                                                            2000WO-US09218
                                                                                                   99US-0128689
99US-0153453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260-261; 322pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.5%;
                                           Kennedy MJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 572; DB 21;
Pred. No. 1.4e-52;
                                                                                                                                                                                                                                                               rhinitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English
                                                                                                                                                                                                                                                               wound infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                           infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295
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RESULT 6
AAU99917
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Best Local
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14-NOV-2000; 2000US-248331P
14-NOV-2000; 2000US-248362P
14-NOV-2000; 2000US-248365P
                                                                                                                                                                                                     autoimmune disorder; leukaemia; immunological disorder; cardiovascular disorder; neurological disorder; cellular proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from Pasteurellaceae. The present sequence is a protein encoded by one such virulence gene. The virulence genes of the present invention may be mutated in order to produce an inactive gene. The inactive virulence gene may in turn be used to produce a vaccine, which is useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Attenuated Pasteurellaceae bacteria comprising mutations in virulence genes, useful as a live attenuated vaccine against bacterial infections
                                                                                                                                                                                                                                                                                                                   07-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                               AAU99917 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                           WO200240656-A2
                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                      67210; glucosyl transferase; haematopoeitic disorder; block
                                                                                                                                                                                                                                                                                   Human 67210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Pages 149-150; 322pp; English.
                                                             14-NOV-2001; 2001WO-US45291.
                                                                                             23-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                             292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDIVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEENRAAVAANLRG-GGNIR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family Pasteurellaceae encompasses several pathogens that infect a evariety of animals. The present invention relates to virulence genes
                                                                                                                                                                                        plood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QYKDVMQYQDQDILNGLFKGGVCYANSRFNFMPTNYAFMANGFASRHTDPLYLDRTNTAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIAVNEKEFESFPVQISYISLATYARLKAAEYLPDNLNKIIYLDVDVLVFNSLEMLWNVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYPNQMIYQDQDILNILFRNKVCYLDCRFNFMPNQLERIXQYHKGKXSNLHSLEK--TTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VNNFLTAACYDSFIENEKSEHKKSISMSDKEYYFNAGVMLFNLDEWRKMDVFSRALDLLA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIDVNPEDFAGFPLNIRHISITTYARLKLGEYIAD-CDKVLYLDTDVLVRDGLKPLWDTD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MNILEVSDDVYAKHLVVAIKSI · INHNEKGISFYIFDLGIKDENKRNINDIVSSYGSEVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIRYKFKYQVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLSARFLRKIY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVVISHYCGPEKAWHADCKHFNVYFYQKILAXXS-----RGXDKERVLSIKTYLKALIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVAVSHYCGSAKPWHRDCTVWGAERFTELAGSLTTVPEEWRG--KLAVPPTKCMLQRWRK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infections such as septicemias, bronchopneumonias, rhinitis
                                                                                                                                                                                        cell disorder; viral disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 AA;
                                                                                                                                                                                                                                                                                   glycosyl transferase domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             302
                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.3%;
                                                                                                                                                                                                                                      blood clotting disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 568; DB 21;
Pred. No. 3.7e-52;
                                                                                                                                                                                                                                                    infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 116;
                                                                                                                                                                                        neurological disorder
                                                                                                                                                                                                                                                                                   consensus sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 302;
                                                                                                                                                                                                                                       cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cc an inability to clear infections (e.g., viral or bacterial infections), cc as well as disorders related to abnormal cellular proliferation or cc disorders of metabolic imbalance (e.g., disorders of lipopolysaccharide constructions), in the providers of metabolic imbalance (e.g., disorders of lipopolysaccharide cc disorders or glycogen synthesis) immunological disorders, cc cardiovascular disorders, neurological disorders, or cellular cc proliferation and/or differentiation disorders, cg., cancer, cell cc motility and adhesion disorders differentiative disorders, red blood cc cell disorders, viral diseases, neurological disorders, red blood cc cell disorders, viral diseases, neurological disorders, red blood cc disorders, path or metabolic disorders alter disorders, kidney cc disorders, disorders of the small intestine, disorders associated with consensus protein trafficking disorders and disorders associated with consensus protein trafficking disorders and disorders associated with consensus sequence y predictive medicine (e.g., diagnostic assays, cc cancent sequence represents a predicted consensus sequence motific cound in the protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-NOV-2000;
30-NOV-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to the DNA and protein sequences of novel isolated 47476, 67210, 49875, 46842, 33201, 83378, 84233, 64708, 85041 or 84234 proteins. The method of the invention is useful for treating a disorder characterised by abberrant activity of 47476, 67210, 49875, 46842, 33201, 83378, 84233, 64708, 85041 or 84234-expressing cell in a subject. The protein molecules can act as novel diagnostic targets and therapeutic agents for controlling aberrant or deficient signal transduction resulting, in e.g., haematopoeitic disorders, including blood clotting disorders, autoimmune disorders, or disorders related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or 84234 polypeptides, useful as reagents or targets for treating diagnosing pain or metabolic, liver, kidney, or cardiovascular disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 6; 298pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-508325/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated 47476, 67210,
253
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                                       SRFNFMPTNYAFMANGFASRHTDPLYLDRTN-TAMPVAVSHYCGS-AKPWHR
                                                                                                                                                                                                                                                                                                                                                                                     DTEIRFHVLDAGISEENRAAVAANLRGGGN--------IRFIDVNPED--F 68
PRYNTQYSNVAYMYYFLKWRHKEKLAKKLLNPTKGNPSIVHYCGAGTKPWHK
                                                                                                                       LINLKKWRRHDIFKMSCEWVEQYK--DVMQYQDQDILNGLFKG-----GVCYAN
                                                                                                                                                                                                               DLGGNWV-GAC-----IDLFVERQEG----YKQKIGMADG----EYYFNAGVL 156
                                                                                                                                                                                                                                                           ESLPLTANMKRRISKATYAREDIQVLLLADLLPDYSKKRVLYLDADVVVKGADLSELLDL
                                                                                                                                                                                                                                                                                                   AGFPLNI---RHISITTYAR-----LKLGEYIADCDK--VLYLDTDVLVRDG-LKPLWDT 117
                                                                                 LINLKKWREENLEKKALELLNEKKEEDVYFYPDQDVLNILFKGKFKSDEIDSIARVLFLP
                                                                                                                                                                     DLGENKILGAVEDLVSNESKFFFVDFWQERAKSRLIEYEQFLYETDGLKVIGSYFNAGVL
                                                                                                                                                                                                                                                                                                                                           EENVKFHILTDGFKEKSRLLVSQ----GDNKKLLETLAPPEFQHFTAIRFYDINTSDELL
                                                                                                                                                                                                                                                                                                                                                                                                                               102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Curtis
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2000US-250176P.
2000US-250327P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49875,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glucksmann
                                                                                                                                                                                                                                                                                                                                                                                                                               33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 330; DB 23; Pred. No. 1.5e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46842, 33201, 83378, 84233,
                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X
                                                                                                                                                                                                                                                                                                                                                                                                                               87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                         253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64708, 85041
                                                                                                                                                                                                                                                                                                                                                                                                                               70;
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                           203
                                                                                                                                                                       192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a method for determining the effect of a test sample on UDP-glucose:glycoprotein glucosyltransferase (UGGT) activity. The method comprises exposing an acceptor substrate for UGGT to a labelled donor in the presence of the test sample and UGGT. The method is useful for determining UGGT activity. In particular, the method is useful in glucosyltransferase assay and kinetics measurement for determining UGGT activity. UGGT is a soluble enzyme of the endoplasmic reticulum which catalyses the addition of a glucose residue onto asparagine-linked oligosaccharides, which are present on incorrectly folded glycoproteins. The present sequence was used in a sequence homology comparison with rat UGGT (see AAF60732 and AAB72436) which was used in the method of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determining the effect of a test sample on UDP-glucose:glycoprotein glucosyltransferase (UGGT), useful for measuring UGGT activity, comprises exposing an acceptor substrate for UGGT to a labeled donor the presence of UGGT -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
Streptococcus pneumoniae; vaccine; screening; protein antigen;
                                                          Streptococcus
                                                                                                                        24-MAY-2000
                                                                                                                                                                                                                                          AAY81561 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tessier
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200112845-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UGGT; UDP-glucose:glycoprotein glucosyltransferase; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Partial GLUT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB72455 standard; Protein; 106 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CANA )
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                                                                                                                                                                                                                                                                                                                                                                                                                151 FNAGVLLINLKKWRRHDIFKMSCEWVEQYKDVMQYQDQDILNGLFKG
                                                                                                                                                                                                                                                                                                                                                                                          60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 IADCDKVLYLDTDVLVRDGLKPLWDTDLGGNWVGACIDLFVE-RQEGYKQKIGMADGEYY 150
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                                                                                                                                                                                                                                                                                                                                                                                    FNAGILLINLNKWKEENIFQKSINWMNKYNNVMKYQDQDILNGICKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-218358/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IKNIEKAIYIDVDTLTNSSLQELWNIDITNYYLAACRDTFIDVKNEAYKKTIGL-EGYSY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig 10; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                          pneumoniae type 4 protein sequence #61.
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                                                                                                                                                                                                                                          Protein;
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46.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
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Pred. No. 6.3e-22;
4; Mismatches 31
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RESULT 9
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                         specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antiinflammatory properties. The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be used in vaccines and in diagnostic assays. The proteins and nucleotides can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and meningitis. AAA05591 to AAA05614 represent primers used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Streptococcal protein, useful as a vaccine, for dia
pneumococcal diseases and for screening agents capable
or inhibiting expression of the protein
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19-MAR-1999;
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pneumococcal disease.
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                                                                                                                                                                                                                                                                                                         3 IVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEE-----NRAAVAANLRGGGN 57
                                                                                                                                                                 DLGGNWVGACIDLEVERQEGYKQKIGMADGEYYFNAGVLLINLKKWRRHDIFKMSCEWVE 177
                                                                                                 QYKDVMQYQDQDILNGLFKGGVCYANSRFNFMPTNYAFMANGFASRHTDPLYLDRTNTAM 237
PPTIVHYASHDKPWN----TYSISRLREL
                                PVAVSHYCGSAKPWHRDCTVWGAERFTEL 266
                                                                 EQNQVVHLGDQSILNIYFEDNWLALDKTYNYMVGIDIYHLAQECERLDD-
                                                                                                                                   DLKGYSIGAVDDVYA--YEGRKSG-----FNTGMLLMDVAKWKEHSIVNSLLELAA 165
                                                                                                                                                                                                     IRSVHIDKELFESYKTG-PHINYASYFRFFATE-VVESDRVLYLDSDIIVTGELATLFEI 116
                                                                                                                                                                                                                                     IRFIDVNPEDFAGFPLNIRHISITTYARLKLGEYIADCDKVLYLDTDVLVRDGLKPLWDT 117
                                                                                                                                                                                                                                                                         IVLAADNAYLIPLETTIKSV--LYHNRDVDFYILNSDIAPEWFKLLGRKMEVVN----ST 58
                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to AAY81679 represent specifically claimed protein sequences from Streptococcus pneumoniae. AAA05407 to AAA05590 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 78; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              399 AA;
                                                                                                                                                                                                                                                                                                                                            Conservative
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99US-0125164.
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27.5%;
                                                                                                                                                                                                                                                                                                                                            42;
                                                                                                                                                                                                                                                                                                                                          Score 233; DB 21;
Pred. No. 5.2e-16;
2; Mismatches 115
240
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capable of anta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      host cell. The method comprises introducing into the host cell a nucleic acid encoding the glycosyltransferase and incubating the host cell under conditions appropriate for expression of the glycosyltransferase, where the host cell substantially lacks a protease that cleaves polypeptides between two consecutive positively charged amino acid residues. The glycosyltransferase can be used in in vitro production of oligosaccharide structures which are potential therapeutic agents for use in the manipulation of cell-cell recognition events, particularly adhesion of bacteria and viruses to mammalian cells and leukocyte-endothelial cell interaction through selectins in inflammation. The method provides more readily recoverable active glycosyltransferases than prior art methods involving mammalian glycosyltransferases. The present sequence represents a C-terminal peptide from Neisseria meningitidis lgtC from the present invention.
                                                          Streptococcus agalactiae
                                                                                                                 Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expressing high levels of glycosyltransferases - comprises use either host cells deficient in proteolytic enzymes or modified glycosyltransferase genes deleted in a proteolytic recognition
                                                                                                                                                                                                                                                      Streptococcus
                                                                                                                                                                                                                                                                                                                    02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                  ABP28548
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP28548 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 8; 61pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 ERFTELAGSLTTVPEEWRGKLAVP----PTKCMLQRWRKKLSARFLRKIY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERFTELAGSLTTVPEEWRGKLAVPHRMFSTKRMLQRWRRKLSVRFLRKIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 has been developed of expressing a glycosyltransferase in a l. The method comprises introducing into the host cell a nucleic oding the glycosyltransferase and incubating the host cell under
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                                                                                                                                                                                                                                                      polypeptide SEQ
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                                                                                                                                                                                                                                                      ID NO 6272.
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RESULT 11 AAG15767

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                                                                                                                                                                                                                                                                                                                                                                                                                                                               streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus/GBS), given i the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to determine whether a compound binds to [I]. A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein - \ 
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 3790-3791; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Telford J,
Tettelin H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-OCT-2000;
24-NOV-2000;
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PNII--HFLTSDKPWNEN----SVARFREL
                               MPVAVSHYCGSAKPWHRDCTVWGAERFTEL
                                                                                            YKDVMQYQDQDILNGLFKGGVCYANSRFNFMPTNYAFMANGFASR--HTDPLYLDRTNTA
                                                                                                                                FKGYYLAAVKDPHKNEEGG
                                                                                                                                                LGGNWVGACIDLFVERQEGYKQKIGMADGEYYFNAGVLLINLKKWRRHDIFKMSCEWVEQ
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)B; ABN69179.
                                                              LHRVVKTGDQSILN----IVCH--NRWLSLNKTWNFQTYDVVSRYNHRSYLYLNIENRT
                                                                                                                                                                                               VKIYNY-----DIAHLTTFLTVSTWFRLFLADYIPS-SRVLYLDSDIIVNTNLDYLFELD
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INST GENOMIC RES
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; 2001GB-0005640.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins
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thaliama: 2000EP-0301439. 9908-0122180. 9908-0122180. 9908-0122783.	(first entry) thaliana protein fragment SEQ ID NO: 16147. tification; signal transduction pathway; metabolic pathway; no assay; genetic mapping; gene expression control; promoter; sequence.
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                                                                                                                                              IVFAADDNYAAYLCVAAKSV--EAAHPDTEIRFHVLDAGISEENR--AAVAANLRGGGNI: | | | | : : | | : : | | : : : |
                 INLKKWRRHDIFKMSCEWVEQYKDVMQYQDQDILNGL-----FKGGVCYANSRFNEMPT
                                               VVDDIAKLWKTSLGSRIIGAPEYCYANFTKYFTGGFWSEERFSGTFRGRKPCYFNTGVMV
                                                           VRDGLKPLWDTDLGGNWVGA---CIDLFVERQEGYKQKIGMADGEY-----YFNAGVLL
      IDLKKWRRGGYTKRIEKWMEIQRRERIYE----LGSLPPFLLVFAGHVAPISHRWN----
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hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
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----QHGLGGDNVRGSCRDLHP------GPVSLLHWSGSGKPWIR 309
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Pred. No. 2.7e-12;
38; Mismatches 104;
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                                                                                                                                                                                       comprising GBS polynucleotides or polypeptides can be used as vaccines and for the treatment or prophylaxis of GBS infection. The polynucleotides and polypeptides can also be used in the detection of GBS and for screening DNA encoding bacterial cell envelope associated or secreted antigens in gram positive bacteria. AAA05873 to AAA05941 represent primers used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                    Claim 1;
                                                                                                                                                                                                                                                                                                                                                                               New Group B Streptococcus protein, useful as vaccine, for diagnosis of Streptococcal infections and for screening of antibodies or affibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JUL-1998;
19-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JUL-1999;
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antibody; affibody; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Group B Streptococcus; Streptococcus agalactiae; protein antigen; vaccine; screening; immunogen; detection; diagnosis; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Group B Streptococcus protein
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                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                        AAA05803 to AAA05872 encode proteins, polypeptides and peptides in AAY91275 to AAY91343) isolated from Group B Streptococcus (Gi known as Streptococcus agalactiae. The GBS polynucleotides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Le Page RWF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MICR-) MICROBIAL TECHNICS LTD
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                                                                                                                                                                                                                                                                               polypeptides have antibacterial activity. Immunogenic compositions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRDGLKPLWDTDLGGNWVGA---CIDLFVERQEGYKQKIGMADGEY-----YFNAGVLL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----QHGLGGDNVRGSCRDLHP------GPVSLLHWSGSGKPWIR
                                                                                                                                                                                                                                                                                                                                                                                                                           2000-195299/17.
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            IRFIDVNPEDFAGFPLNIRHISITTYARLKLGEYIADCDKVLYLDTDVLVRDGLKPLWDT 117
                                                                        IVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEENRAAVAANLRGGGN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDLKKWRRGGYTKRIEKWMEIQRRERIYE----LGSLPPFLLVFAGHVAPISHRWN----
                                             VVLAGDYSYIRQIETTLKSLCVYHENLSI--FIFNQDIPQEWFLAMKDRVGQTGNQIQDV 64
                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                    Fig 1; 123pp;
                                                                                                                                                              313
                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wells JM,
                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98GB-0016335.
99US-0125163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-GB02444
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                                                                                                                 11.9%;
28.1%;
                                                                                                                                                                                                                                                                                                                                                      English
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                                                                                                                 Score
Pred.
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                                                                                                     Mismatches
                                                                                                                 197;
No. 2.
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                                                                                                                   DB 21;
.7e-12;
103;
                                                                                                                                Length 313;
                                                                                                      Indels
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                                                                                                      42;
                                                                                                                                                                                                                                                                                                           (GBS),
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B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antilnflammatory; infection; vaccine; meningitis; gene therapy.
                                                            Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-2002
           acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                      The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for
                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                       New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-352536/38
N-PSDB; ABN69181.
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24-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP28550 standard; Protein; 398
                                                                                                                                                                                                                                                                                                                                                                                                                                    Tettelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Telford J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-OCT-2001;
                                                                                                                                                            the treatment or prevention of infection or disease caused by
                                                                                                                                                                                                                                                                                                                        for detecting a compound that binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHIR-) CHIRON SPA. (GENO-) INST GENOMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPITPLP-KIIHYISGIKPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNQKEIENANEGDQTILNRMFENQVIYLDDTYNFQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QYKDVMQYQ----DQDILNGLFKGGVCYANSRFNFMPTNYAFMANGF----ASRHTDPLYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLFHDHLSPKWENKKLN--HINYMTYARYFIPQYIS-ADTVLYLDSDLVVTTNLDNLFQI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                    Η;
                                                                                                                                                                                                                                                                                      Page 3791; 4525pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 2000GB-0026333.
; 2000GB-0028727.
; 2001GB-0005640.
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proteins
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Best Local
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24-NOV-2000;
07-MAR-2001;
The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory
                                                                                                                                                                                                                                                                                                                                                                               Telford J,
Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial;
                                                                                                                                                                                          New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                WPI; 2002-352536/38.
N-PSDB; ABN68042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiinflammatory; infection; vaccine; meningitis; gene therapy.
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                                                                                                                                   Claim 1; Page 3555; 4525pp; English
                                                                                                                                                                                       for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIR-) CHIRON SPA. (GENO-) INST GENOMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-OCT-2001; 2001WO-GB04789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTNTAMPVAVSHYCGSAKPW 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNQKEIENANEGDQTILNRMFENQVIYLDDTYNFQ-----IGFDMGAAIDGHKFIFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLGGNWVGACIDLFVERQEGYKQKIGMADGEYYFNAGVLLINLKKWRRHDIFKMSCEWVE 177
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; 2000GB-0028727.
; 2001GB-0005640.
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28.1%;
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Pred. No. 3.8e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid encoding (I) may be used to recombinantly produce (I) and may used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic
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ALIGNMENTS	US-09-521-780-3	US-09-521-780-2	US-08-633-770A-1	US-09-376-330-34	US-08-836-325-15	US-09-208-716-3	US-08-726-320-3	US-09-376-330-16	US-09-510-791-1	US-09-542-331-1	PCT-US95-10661A-5	us-08-296-791-5	US-08-473-446-4	US-08-413-118-4	US-08-220-151-4	US-09-073-297-5	US-09-434-066-23	US-08-961-083-70
	Sequence 3, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 34, Appl	Sequence 15, Appl	ω	Sequence 3, Appli	16,	Sequence 1, Appli	1,	Sequence 5, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 5, Appli	Sequence 23, Appl	Sequence 70, Appl

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RESULT 1
US-08-312-387B-4
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Sequence 4, Application US/08312387B
Patent No. 5545553
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GOTSCHICH, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING T
                                            Query Match
                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION UNMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELEPHONE: 201 487-5800
TELEPHONE: 201 487-5800
TELEPHAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentLD Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,387B
FILING DATE: July 7, 1994
CLASSIFICATION: 435
                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 07601
                    Local
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100.0%; Score 1657; DB 1; ilarity 100.0%; Pred. No. 9.9e-171; Conservative 0; Mismatches 0;
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                                                                                                                                     ; MOLECULE TYPE: protein US-08-683-426-4
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                                                                      Matches
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Best Local Similarity
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                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DALL.
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/312,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 411 Hacken
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                       NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                 1 MDIVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEENRAAVAANLRGGGNIRF 60
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                                                                    Conservative
                                                                                                                                                                       linear
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                                                                                100.0%;
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                                                                                  Score 1657; DB 1; Pred. No. 9.9e-171;
                                                                    Mismatches
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US-08-683-458-4
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                                                                 Matches 306;
                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                 TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/683 AFT FILING DATE:

CLASSITETION NUMBER: US/08/683 AFT FILING DATE:

CLASSITETION NUMBER: US/08/683 AFT CLASSITETION.
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: GL
TITLE OF INVENTION: OL
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acid
                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New COUNTRY: U. ZIP: 07601
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                                                                                                                                                                   TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                    TELEPHONE: 201 %C,
                                                                                                                                                                                                                                                                                                                   NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
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            1 MDIVEAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEENRAAVAANLRGGGNIRF 60
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MDIVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEENRAAVAANLRGGGNIRF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411 Hackensack Avenue
                                                                                                                                                                                                  306 amino acids
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VENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF

VENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                 Conservative
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                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                      600-1-095A
                                                                               Score 1657; DB 1; Pred. No. 9.9e-171;
                                                                Mismatches
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                                                                                                 Length
                                                                 Indels
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                                                                      US-08-878-360-4
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US-08-878-360-4
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Best Local Sir
Matches 306;
                                    Query Match
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                                                                                                                                                     TELEX: 133521
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,360
FILING DATE: 18-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/3:
FILING DATE: September 2:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David
                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                            NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095B
                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 07601
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CITY: Hackensack
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                                                                                                                        TYPE:
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                                                                                                                                         LENGTH:
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                  Similarity
                                                                                                      amino acid
)GY: linear
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                                                                                                                                     306 amino acids
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N: 435
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              Score 1657; DB 2;
Pred. No. 9.9e-171;
   Mismatches
                                Length
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                                                                                                                                       REFERENCE/DOCKET NUMBER: 7188-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-990
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
   Matches 306; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08478140B Patent No. 6127153
                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Laura A. COTUZZI
REGISTRATION NUMBER: 30,74
                                                                            TYPE: amino :
TOPOLOGY: li:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BUCZALA, STEPHANIE L.

TITLE OF INVENTION: METHOD OF TRANSFERRING AT LEAST TWO
TITLE OF INVENTION: SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSFERASE,
TITLE OF INVENTION: POLYGLYCOSYLTRANSFERASE AND GENE ENCODING A
TITLE OF INVENTION: POLYGLYCOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: JOHNS APPLICANT: ROTH, APPLICANT: BUCZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
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STREET: 1155 Avenue of the Americas
                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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100.0%; ilarity 100.0%; Conservative 0
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Score 1657; DB 3; Pred. No. 9.9e-171; Mismatches 0;
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                              Length
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US-09-333-412-4
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                                                           US-09-333-412-4
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Patent No. 6342382
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil (
  Best Local Similarity
                    Query Match
                                                                                                                                                                       TELEX: 133521
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Jun-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/312,387 FILING DATE: July 7, 1994
                                                                                                                                                                                                                                                                                                                NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Hackensack
                                                                                                                                                           LENGTH: 306 amino acids
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100.0%;
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Score 1657; DB 4; Pred. No. 9.9e-171;
                Length 306;
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RESULT 7
US-09-338-943-4
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                                                                                     TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 4:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: IMB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 FLRKIY 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 VSHYCGSAKPWHRDCTVWGAERFTELAGSLTTVPEEWRGKLAVPPTKCMLQRWRKKLSAR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 DVMQYQDQDILNGLFKGGVCYANSRFNFMPTNYAFMANGFASRHTDPLYLDRTNTAMPVA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GNWVGACIDLFVERQEGYKQKIGMADGEYYFNAGVLLINLKKWRRHDIFKMSCEWVEQYK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                  TYPE: amino acid TOPOLOGY: linear
                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 IDVNPEDFAGFPLNIRHISITTYARLKLGEYIADCDKVLYLDTDVLVRDGLKPLWDTDLG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSHYCGSAKPWHRDCTVWGAERFTELAGSLTTVPEEWRGKLAVPPTKCMLQRWRKKLSAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROTH, STEPHEN
BUCZALA, STEPHANIE L.
SUZGALA, STEPHANIE TRANSFERASE AND GENE ENCODING A NVENTION: POLYGLYCOSYLTRANSFERASE
SUVENTION: POLYGLYCOSYLTRANSFERASE
                                                  306 amino acids
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                                                                                                                         (212) 869-9741/8864
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of the Americas
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                                                                                                                                                                                            30,742
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RESULT 9
US-09-376-330-27
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US-09-376-330-28
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   Sequence 27, Application US/09376330 Patent No. 6399321
                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 28
LENGTH: 106
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21
Patent No.
                                                                                                                                                                                                                                                                                         Query Match
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APPLICANT: Dignard, Daniel
APPLICANT: Bergeron, John J.M.
APPLICANT: Bergeron, John J.M.
APPLICANT: Thomas, David Y.
TITLE OF INVENTION: Wethod for screening for
TITLE OF INVENTION: UDP-glucose:glycoprotein glucosyltransferase (UGGT) activity
TITLE OF INVENTION: and nucleic acid encoding for UGGT
FILE REFERENCE: 2139-9"US"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/376,330
CURRENT FILING DATE: 1999-08-18
NUMBER OF SEQ ID NOS: 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVMQYQDQDILNGLFKGGVCYANSRENEMPTNYAFMANGFASRHTDPLYLDRTNTAMPVA 240
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o. 6399321
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                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                     35.2%; Score 583; DB 4; 1
100.0%; Pred. No. 2.1e-55;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                       Length 106;
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APPLICANT: Dignard, Daniel
APPLICANT: Bergeron, John J.M.
APPLICANT: Thomas, David Y.
APPLICANT: Thomas, David Y.
TITLE OF INVENTION: Method for screening for
TITLE OF INVENTION: Method for screening for
TITLE OF INVENTION: and nucleic acid encoding for UGGT
TITLE OF INVENTION NUMBER: US/09/376,330
CURRENT APPLICATION NUMBER: US/09/376,330
CURRENT APPLICATION DUMBER: US/09/376,330
CURRENT FILING DATE: 1999-08-18
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 27
LENGTH: 106
TYPE: PRT
ORGANISM: Artificial Sequence
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US-08-961-083-200
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                                                                     TELEFAX: (301) 309-85: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20850
COMPUTER READABLE FORM:
                            SEQUENCE CHARACTERISTICS:
LENGTH: 674 amino acids
                                                                                                                      REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 FNAGVILINLKKWRRHDIFKMSCEWVEQYKDVMQYQDQDILNGLFKG 197
||||:||||||||:|||
60 FNAGILLINLNKWKEENIFQKSINWMNKYNNVMKYQDQDILNGICKG 106
                                                                                                                                                                                                                                                                                                                                COMPUTER: HP Vectra 486/33 inch, 1.4Mb OPERATING SYSTEM: MSDOS Version 6.2 SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 9410 Ke
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 IADCDKVLYLDTDVLVRDGLKPLWDTDLGGNWVGACIDLEVE-RQEGYKQKIGMADGEYY 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 16.9%; Score 280; DB 4;
Local Similarity 46.7%; Pred. No. 1.1e-22;
                                                                                      TELEPHONE: (301)
TELEFAX: (301) 30
                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/961,08:
STRANDEDNESS:
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                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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single
                                                                                  309-8512
                                                                                                       309-8504
                                                                                                                                                        36,373
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Gaps

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RESULT 12
US-09-073-297-6
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US-09-376-330-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dignard, Daniel
APPLICANT: Bergeron, John J.M.
APPLICANT: Bergeron, John J.M.
APPLICANT: Bergeron, John J.M.
APPLICANT: Bergeron, John J.M.
APPLICANT: Thomas, David Y.
TITLE OF INVENTION: Method for screening for
TITLE OF INVENTION: UDP-glucose:glycoprotein glucosyltransferase (UGGT) activity
TITLE OF INVENTION: UDP-glucose:glycoprotein glucosyltransferase (UGGT) activity
TITLE REFERENCE: 2139-9"US"
CURRENT FILLING 1319-9"US"
CURRENT FILLING DATE: 199-08-18
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 29
LENGTH: 105
TYPE: PRT
                                                                       Sequence 6, Application US/09073297 Patent No. 6255114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Tessier, Daniel C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 29, Application US/09376330 Patent No. 6399321
                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
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                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                             APPLICANT:
                                                                                                                                                                                                                                             157 LINLKKWRRHDIFKMSCEWVEQY--KDVMQYQDQDILNGL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    493
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                                                                                                                                                                                                     63 IIDFESWRKQNITEKVINFINEHPDEDFLVLHDQDALNAI 102
                                                                                                                                                                                                                                                                                                                   97 KVLYLDTDVLYRDGLKPLWDTDLGGNWVGACIDLFVERQEGYKQKIGMADGEYYFNAGVL 156 ::::|: | | | | | | : | ::
                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 28.0
mes 28; Conservative
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                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSCEWVEQYKDVMQYQDQDILNGLFKGGVCYANSRFNFMPTNYAFMANGFASRHTDPLYL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNPEDFAGFPLNIR------HISITTYARLKLGEYIADCDKVLYLDTDVLVRDGL 111
                                                                                                                                                                                                                                                                                          RMIYIDCDALVLEDISKLWDLDIAPYTVAAVED----AGQHERLKEMNVTDTGKYFNSGIM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----AIIHYLSHRKPWKDLAAQTYRE--VWWYYHGLE-WTEL 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLIDVTNEWHDKVDQADQSILNMLFEHKWLELDFDYNHIVIHKQFADYQLPEGQDYP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KRLEKFDSEIINCRVTSEQISCYKSDISYTVFLRYFIADFVQE-DKALYLDCDLVVTKNL 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEENRAAVAANLRGGGNIRFID 62
4
                               LIGHTNER,
                                                                                                                                                                                                                                                                                                                                                                                                      8.5%;
28.0%;
                               JONATHAN EDWARD
                                                                                                                                                                                                                                                                                                                                                                                27;
                                                                                                                                                                                                                                                                                                                                                                                                  Score 140.5; DB 4
Pred. No. 1.3e-07;
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                                                                                                                                                                            US-09-376-330-25
                                                                                                              Sequence 25, Application US/09376330 Patent No. 6399321 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                     APPLICANT: Tessier, Daniel C. APPLICANT: Dignard, Daniel APPLICANT: Dignard, Daniel APPLICANT: Bergeron, John J.M. APPLICANT: Thomas, David Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/852615
FILING DATE: MAY 7, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MAJARIAN, WILLIAM R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-973-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 9:
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/073,297
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
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MEDIUM TYPE: DISKETTE, 3.50
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                                                                                                                                                                                                                                                       283
                                                                                                                                                                                                                                                                                                                                                                                                          198
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                                                                                                                                                                                                                                                                                                                                                                  233 TNTAMPVAVSHYCGS-AKPWHRDCTVWGAERFTELAGSLTTVPEEWRGKLAVPPTKCMLQ 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: no
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95
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STATE: DELAWARE
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STREET: 10
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                                                                                                                                                                                                                                                       RW 284
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                                                                                                                                                                                                                                                                                                                                  ----VKVVHYCAAGSKPW---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   not relevant
                   David Y.
Method for screening
 UDP-glucose:glycoprotein glucosyltransferase (UGGT) activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.0%; score 132; DB 4; Length 328; 23.1%; Pred. No. 5.6e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                          ----EQYKPIPNVYNLVL-AMLWRHPENVDLDQ
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                                                                                                                                                                                                                                                                                                                                --DIKMLVK 282
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RESULT 15
US-09-376-330-24
; Sequence 24, Application US/09376330
; Patent No. 6399321
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US-09-376-330-30
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US-09-376-330-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/376,330
CURRENT FILING DATE: 1999-08-18
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30
LENGTH: 121
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/376,330
CURRENT FILING DATE: 1999-08-18
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 28.3 Matches 36; Conservative
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APPLICANT: Thomas, David Y.
TITLE OF INVENTION: Method for screening for
TITLE OF INVENTION: UDP-glucose:glycoprotein glucosyltransferase (UGGT) activity
TITLE OF INVENTION: and nucleic acid encoding for UGGT
FILE REFERENCE: 2139-9"US"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: and nucleic acid encoding FILE REFERENCE: 2139-9"US"
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Q48480-K. p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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113 DIMNKVF 119
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                                                                                                                                                                                                                                                 148 EY-----YFNAGVLLINLKKWRRHDIF-----KMSCEWVEQYKDVMQYQDQ 188
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                                                                                                                                                                                                                                                                                                                                  96 DKVLYLDTDVLVRDGLKPLWDTDLGGNWVGACIDLFVERQEGYKQKIGMA------DG 147
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                                                                                                                                                                                                                                                                                          DKVVFIDSDTVVKADLGELLDVPLGNNLVAAVKDIVM---EGFVKFSAMSASDDGVMPAG 61
                                                                                                                                                                                                             EYLQKTLNNNPDEYFQAGIIVFNVKQMVEENTFAELMRVLKAKKYW
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28.3%; Pre
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                                                                                                                                                                                                                                                                                                                                                                         Score 121.5; DB 4;
Pred. No. 1.8e-05;
20; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 121;
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Search completed: December Job time: 12.3901 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQ ID NO 24
; LENGTH: 110
; TYPE: PRT
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tessier, I
APPLICANT: Dignard,
APPLICANT: Bergeron
APPLICANT: Thomas, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dignard, Daniel
APPLICANT: Bergeron, John J.M.
APPLICANT: Thomas, David Y.
APPLICANT: Thomas, David Y.
TITLE OF INVENTION: Method for screening for
TITLE OF INVENTION: UDP-glucose:glycoprotein
TITLE OF INVENTION: and nucleic acid encodin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/376,330 CURRENT FILING DATE: 1999-08-18 NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: UDP-glucose:glycoprotein glucosyltransferase (UGGT) activity TITLE OF INVENTION: and nucleic acid encoding for UGGT FILE REFERENCE: 2139-9"US"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                               144 MADGEYYFNAGVLLINLKKWRRHDIFKMSCEWVEQYKDVMQ--YQDQDILN 192
                                                                                                                                                                                                                            97 KVLYLDTDVLVRDGLKPLWDTDLGGN-------WVGACIDLFVERQEGYKQKIG 143
                                                                                       57 LVSG--YFNAGFILIXIPLWTAENISKKAIEMLKDPEVVQRITHLDQDVLN 105
                                                                                                                                                                                6 KVLYLDADIACKGSIQELIDLNFAENEIAAVVAEGELEWWTNARLSLATP------G 56
                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Daniel C.
                                                                                                                                                                                                                                                                                                6.9%;
28.8%;
                   2002, 12:03:14
                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                Score 115; DB 4; Pred. No. 7.7e-05;
                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                   Length 110;
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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                    NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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        1657
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1: /cgn2_6/ptodata/1/pubpaa/U
2: /cgn2_6/ptodata/1/pubpaa/U
3: /cgn2_6/ptodata/1/pubpaa/U
4: /cgn2_6/ptodata/1/pubpaa/U
5: /cgn2_6/ptodata/1/pubpaa/U
6: /cgn2_6/ptodata/1/pubpaa/U
6: /cgn2_6/ptodata/1/pubpaa/U
9: /cgn2_6/ptodata/1/pubpaa/U
10: /cgn2_6/ptodata/1/pubpaa/U
11: /cgn2_6/ptodata/1/pubpaa/U
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12: /cgn2_6/ptodata/1/pubpaa/U
13: /cgn2_6/ptodata/1/pubpaa/U
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length: 2000000000
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1657
1 MDIVFAADDNYAAYLCVAAK.....KCMLQRWRKKLSARFLRKIY 306
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. /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
. /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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. /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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10
                       10 US-09-881-752A-320
US-09-829-482-6
10 US-09-925-299-864
10 US-09-992-598-171
10 US-09-989-722-171
10 US-09-989-727-171
10 US-09-989-727-171
10 US-09-989-727-171
10 US-09-989-732-171
10 US-09-989-732-171
10 US-09-989-732-171
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10 US-09-991-073-171
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US-09-765-272-200
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Sequence 4, Appli
Sequence 200, App
Sequence 320, App
Sequence 6, Appli
Sequence 171, App
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4.4	4.4	4.4	4.5	4.5	4.5	4.5	4.6	4.6	4.6	4.6	4.6	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.9	4.9		5.0		5.9	7.1
493	342	333	1169	416	316	316	1066	1066	495	495	311	536	536	566	2310	1019	811	593	437	389	389	756	394	346	281
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US-09-815-242-12052	US-09-911-150-4	US-09-829-482-3	US-09-771-161A-222	US-09-971-536-60	US-09-954-314-10	US-09-765-272-156	US-09-280-197-5	US-09-423-126-3	US-09-815-242-11716	US-09-815-242-5040	US-09-981-876-191	US-09-815-242-12978	US-09-815-242-12372	US-09-829-482-5	US-09-995-542-10	US-09-434-066-23	US-09-895-382-32	US-09-815-242-12306	US-09-765-272-70	US-10-007-693-112	US-10-036-507-15	US-09-745-763-142	US-10-036-507-2	US-09-829-482-2	US-09-895-913A-282
Sequence 12052, A	Sequence 4, Appli		Sequence 222, App	Sequence 60, Appl		156	Sequence 5, Appli	Sequence 3, Appli	Sequence 11716, A	Sequence 5040, Ap	Sequence 191, App		Sequence 12372, A	5, 2	10,	-	Sequence 32, Appl	1230	Sequence 70, Appl	112,	Sequence 15, Appl	142,	2	e 2, A	Sequence 282, App

ALIGNMENTS

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                           APPLICATION NUMBER: 08/312,387
FILING DATE: July 7, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esc.
                                                                                                                                                                                                                                                                         CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Jun-1999
FILING DATE: 15-Jun-1999
                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible operating system: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, V CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/007,267
FILING DATE: 03-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New Jersey COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 411 Hackensack Avenue CITY: Hackensack
                                                                                                                                                     NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1-095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 07601
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Klauber & Jackson
                  LENGTH: 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OLIGOSACCHARIDES, AND GENES ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                            Version #1.25
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TOPOLOGY: linear;
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MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: S
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US-09-765-272-200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                             TELEFAX: (301) 309-85
INFORMATION FOR SEQ ID NO: 200:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
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hes 306;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \vdash
                                                                                                                                                                                                                                                                                                       COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                   APPLICATION NUMBER: 08/961,083 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNWYGACIDLFYERQEGYKQKIGMADGEYYFNAGYLLINLKKWRRHDIFKMSCEWYEQYK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSHYCGSAKPWHRDCTVWGAERFTELAGSLTTVPEEWRGKLAVPPTKCMLQRWRKKLSAR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVMQYQDQDILNGLEKGGVCYANSRENEMPTNYAFMANGFASRHTDPLYLDRTNTAMPVA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNWVGACIDLFVERQEGYKQKIGMADGEYYFNAGVLLINLKKWRRHDIFKMSCEWVEQYK 180
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                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Rockville
STATE: Maryland
STRANDEDNESS:
              TYPE: amino acid
                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                             ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Human Genome Sciences,
                                 LENGTH: 674 amino acids
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                                                                                                                                                                                                                                                                                                                                                                          Diskette, 3.50 inch, 1.4Mb storage
                                                                                  309-8512
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                                                                                                    309-8504
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Pred. No. 6.2e-161;
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; molecule Type: protein; sequence Description: Seq ID No: US-09-765-272-200
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; Sequence 320, Application US/09881752A
; Patent No. US20020115078A1
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LENGTH: 372
TYPE: PRT
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/833,457
PRIOR FILING DATE: 1997-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Identification of Polynucleotides TITLE OF INVENTION: Encoding No. US20020115078A1el HTITLE OF INVENTION: Genome FILE REFERENCE: 06132/041002
                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 370
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kleanthous, Harold APPLICANT: Al-Garawi, Amal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Helicobacter
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 148
                                     127
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                                                                                                                                                L---RGGGNIRFIDVNPEDFAGFP-----LNIRHISITTYA------RLKLGE
                                    LFPQYDKIIMFDADTLFLNDVSESFFIPLDGYYFGAAKDFASDKSPKHFQIVREKDPRQA 186
                                                                      YIADCDKVLYLDTDVLVRDGLKPLWDTDLGGNWVGACIDLFVERQEGYKQKIGMADG---
                                                                                                          LAPFSAFSSLEFLDISTPNLHATPIEPSAIDKINEAFLQLNIYAKTRFSKMVMCRLFLAS 126
                                                                                                                                                                                  IVIAFDNHYAMPAGVSLYSMLACAKTEHPQSQNDSEKLFYKIHCLVDNLSLENQSKLKET 66
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Oomen, Raymond P.
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25.1%;
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Pred No. 3e-08;
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STRANDEDNESS: not relevant ropology: linear sequence trype: peptide sequence description: SEQ ID NO: 6: US-09-829-482-6
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                                                                                                                                                                                                      Query Match
                                                                                                                                                                     Matches
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     182
                                  152 PQYDIGYCQQRPDEVAWPERELGPPPPLYFNAGMFV-----HE-----PGLGTAKD 197
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                                                                                                                                                                                   Local
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MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/852615
PILING DATE: MAY 7, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 302-992-4926
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LIGHTNER, JONATHAN EDWARD
TITLE OF INVENTION: STARCH BIOSYNTHETIC ENZYMES
                                                                                                VINYSKLRIWEFV-EYERMVYLDADIQVFDNIDHLFDLDKGAFY--AVKDCFCEKTWSHT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                               ---QEGYKQ----KIGMADGE-----YYFNAGVLLINLKKWRRHDIFKMSCEWVEQYKD 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT-----LACY--QKVLILPYIYNTHPFMAN---QKRFIP---DKKE----IVMLHFYFV 289
                                                                                                                                                                                 h 8.0%; Score 132; DB 10;
Similarity 23.1%; Pred. No. 8.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: MAJARIAN, WILLIAM R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1083-B
                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/829,482 FILING DATE: 10-Apr-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET
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   -YQDQDILNGLFKGGVCYANSRFNFMPTNYAFMANGFASRHTDPLYLDR 232
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US-09-925-299-864
                                                                                                                               GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                Sequence 171, Application US/09992598 Patent No. US20020160384A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 864
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NAME/KEY: SITE
LOCATION: (138)
OTHER INFORMATION: X
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                                                                   APPLICANT:
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                                  APPLICANT:
   APPLICANT:
                  APPLICANT:
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                                                                                                                                                                                                                                                                                                   252 ----HRDCTVW 258
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                                                Ferrara, Napoleone
                                                                                                Baker, Kevin P.
Botstein, David
Gerber, Hanspeter
Gerritsen, Mary E.
                                Fong, Sherman
                                                                   Eaton, Dan
                                                                                 Desnoyers, Luc
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GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                             140 QK----IGMADGEYYFNAGVLLINLKKWRRHDIFKMSCEWVEQYKDVMQYQDQDILNGLF 195
                                                       196 KGGVCYANSRENEMPTNYAFMANGFASRH----TDPLYLDRTNTAMPVAVSHYCGSAKPW 251
                                                                                                                                                                                                                                                                                                   97 KYLYLDTDYLYRDGLKPLWDTDLGGNWVGACID-----LFVERQEG-----YK 139
                                                                                                                                                                                                                                        16 KVIYLDDDVIVQGDIQELYDTTLALGHAAAFSDDCDLPSAQDINRLVGLQNTYMGYLDYR 75
GGGVATSPXLIVF-HGKYSTINPLWHIRHLGWNPDARYSE--HFLQEAKLLHWNGRHKPW 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNTAMPVAVSHYCGS-AKPWHRDCTVWGAERFTELAGSLTTVPEEWRGKLAVPPTKCMLQ 291
                                                                                                                  KKAIKDLGISPSTCSFNPGVIVANMTEWKHQRITKQLEKWMQ--KNV----EENLYSSSL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                          Score 120.5;
Pred. No. 7..
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R APPLICATION NUMBER: 6
R FILING DATE: 1007
R ACCOUNT.
                                                  DR FILING DATE: 1998-06-02
R FILING DATE: 1998-06-02
R FILING DATE: 1998-06-02
R FILING DATE: 1998-06-03
R FILING DATE: 1998-06-03
PR FILING DATE: 1998-06-04
PR FILING DATE: 1998-06-04
R FILING DATE: 1998-06-04
PR APPLICATION NUMBER: 60/08
PR FILING DATE: 1998-06-04
PR FILING DATE: 1998-06-05
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R FAPPLICATION NUMBER: 60/07
R FILING DATE: 1998-03-20
R APPLICATION NUMBER: 60/07
R FILING DATE: 1998-04-28
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E OF INVENTION: Secrete
E OF INVENTION: Acids
REFERENCE: P2730P1C20
APPLICATION IN APPLICATION N
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APPLICATION NUMBER: 60/065186
FILING DATE: 1997-11-12
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FILING DATE: 1997-11-13
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Godowski, Paul J.
Grimaldi, J.Christopher
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art, Timothy A.
                      NUMBER: 60/
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1998-05-07
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PRIOR OR FILING DATE: 1998-06-22
OR APPLICATION NUMBER: 60/09
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R FILING DATE: 1998-06-10
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RESULT 7
US-09-989-722-171
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Best Local S
Matches 48
                                                                                    Sequence 171, Application US/09989722 Patent No. US20020072067A1
                                                   GENERAL INFORMATION:
APPLICANT: Ashkenaz
                APPLICANT:
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APPLICATION NUMBER: 60/091978
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/091982
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APPLICATION NUMBER: 60/090863
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
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APPLICATION NUMBER: 60/
FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/092182
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APPLICATION NUMBER: 60/091633
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APPLICATION NUMBER: 60/090862
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/
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                                                                                                                                                                                            LGSSAGKRYSPQFVKAAKLLHWNGHLKPWGR---
                                                                                                                                                                                                                                                                                  VEQYKDVMQYQDQDILNGLFKGGVCYANSRFNFMPTNYAFMANGFASRHT--DPLYLDR- 232
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                                                                                                                                                                                                                                                                  MK - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                 Ashkenazi, Avi J
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                Baker, Kevin P. Botstein, David
Desnoyers,Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DATE: 1998-07-09
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CURRENT FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/06286
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: 60/065186
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PRIOR APPLICATION NUMBER: 60/065311
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PRIOR FILING DATE: 1997-11-13
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PRIOR APPLICATION NUMBER: 60/075945
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OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087827
OR FILING DATE: 1998-06-03
OR APPLICATION NUMBER: 60/088021
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088025
OR APPLICATION NUMBER: 60/088026
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APPLICATION NUMBER: 60/088167
FILING DATE: 1998-06-05
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FILING DATE: 1998-06-04
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Stewart, Timothy A.
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Williams, P. Mickey
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Kljavin, Ivar J.
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Grimaldi, J.Christopher
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APPLICATION NUMBER: 60/088826 FILING DATE: 1998-06-10 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088824 APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10

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OR APPLICATION NUMBER: 60/091519
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Pred. No. 0.00
38; Mismatches
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-TASYTDVWEKW
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349
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US-09-989-723-171 US-09-989-723-171 ; Sequence 171, Application US/09989723 ; Patent No. US20020072092A1

PRIOR PRIOR

APPLICATION NUMBER: 60/1 APPLICATION NUMBER: 60/1 PTITING DATE: 1998-06-22

APPLICATION NUMBER: 60/ FILING DATE: 1998-06-22

FILING DATE: APPLICATION NUMBER:

1998-06-22

FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-23

60/090349 60/090254 60/090252 60/090246

APPLICATION NUMBER:

60/090355

R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/0
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APPLICATION NUMBER: 60/089908 FILING DATE: 1998-06-18

DR APPLICATION NUMBER: 60/089947

DR FILING DATE: 1998-06-19

RAPPLICATION NUMBER: 60/089948

DR FILING DATE: 1998-06-19

DR APPLICATION NUMBER: 60/089952

DR FILING DATE: 1998-06-19

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DR FILING DATE: 1998-06-17
DR APPLICATION NUMBER: 60/089801
DR FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/089600 FILING DATE: 1998-06-17 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089599 FILING DATE: 1998-06-17

APPLICATION NUMBER:

NUMBER: 60/089653 1998-06-17

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APPLICATION NUMBER:

1998-06-1

FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/ APPLICATION NUMBER: 60/088876 APPLICATION NUMBER: 60/088861 FILING DATE: 1998-06-11 FILING DATE: 1998-06-11 APPLICATION NUMBER:

APPLICATION NUMBER: 60/

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GENERAL INFO
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TITLE OF INVENTION: Secreted and Transmembrar
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: PZ730P1C62
CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19
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OR APPLICATION NUMBER: 60/08

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OR FILING DATE: 1998-06-02

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Botstein, David
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Godowski, Paul
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R APPLICATION NUMBER: 60/090694
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APPLICATION NUMBER: 60/091626
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APPLICATION NUMBER: 60/090542
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38; Mismatches
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/062250
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C65
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Baker, Kevin P.
Botstein, David
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Williams, P. Mickey
Wood, William I.
Zhang, Zemin
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Gerritsen, Mary E
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Roy, Margaret Ann
Stewart, Timothy A.
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Kljavin, Ivar J.
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Stewart, Timothy A.
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Kljavin, Ivar J
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Botstein, David
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P273091C8
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                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/990,442
CURRENT FILING DATE: 2001-11-14
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                                     FILING DATE: 1997-11-12
APPLICATION NUMBER: 60/065311
FILING DATE: 1997-11-13
APPLICATION NUMBER: 60/066770
FILING DATE: 1997-11-24
                                                                                                                       APPLICATION NUMBER: 60/049787
FILING DATE: 1997-06-16
APPLICATION NUMBER: 60/062250
FILING DATE: 1997-10-17
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FILING DATE: 1997-11-12
            APPLICATION NUMBER: 60/075945 FILING DATE: 1998-02-25
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l Similarity 20.4%;
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Godowski, Paul J.
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FILING DATE: 1998-06-18 APPLICATION NUMBER:

60/089908

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APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18

FILING DATE:

NUMBER: 60/089801 1998-06-18

FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089653

APPLICATION NUMBER: FILING DATE: 1998-00 FILING DATE: 1998-06-

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PRIOR

APPLICATION NUMBER: 60/090254 APPLICATION NUMBER: 60/090252 FILING DATE: 1998-06-22 FILING DATE: 1998-06-22 APPLICATION NUMBER:

APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-19

60/090246 60/089952

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nuc.
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730D1C17
CURRENT APPLICATION NUMBER: US/09/991,163
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/06231
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
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Pred. No. 74;
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ALIGNMENTS

R; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Reference number: A64000; MUID:95350630; PMID:7542800
A; Accession: C64146 hypothetical protein HI0259 - Haemophilus influenzae (strain Rd KW20) C;Species: Haemophilus influenzae C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999 C;Accession: C64146 RESULT C64146 QΥ Дb Qy 밁 20 A;Molecule type: DNA A;Residues: 1-220 <TIGR> A;Cross-references: GB:L42023; TIGR:HI0259; GB:U32711; NID:g1573214; PIDN:AAC21924.1; A; Status: nucleic acid sequence not shown; translation not shown Matches Query Match Best Local 157 119 39 LGGNWVGACIDLFVE-RQEGYKQKIGMADGEYYFNAGVLLINLKKWRRHDIFKMSCEWV 176 ITNYYLAACRDTFIDVKNEAYKKTIGL-EGYSYFNAGILLINLNKWKEENIFQKSINWM FFLPVCESDFQNFPKTIDYISLATYARLNLTKYIKNIEKAIYIDVDTLTNSSLQELWNID MNIIFSSDHYYAPYLAVSIFSIIKNTP-KKINFYILDMKINQENK-TIINNLASAYSCKV 96 72; Similarity Conservative 21.1%; 39; Score 349; DB Pred. No. 3.2e 39; Mismatches DB 2; .2e-23; 62; Length 220; Indels 9 Gaps 214 156 59 5

general stress protein gspA - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 06-Jan-1994 #sequence_revision 24-Feb-1995 #text_change 08-Dec-2000
C;Accession: S16423; S39667; PS0148; A69638
R;Glaser, P.; Kunst, F.; Debarbouille, M.; Vertes, A.; Danchin, A.; Dedonder, R.
DNA Seq. 1, 251-261, 1991
A;Title: A gene encoding a tyrosine tRNA synthetase is located near sacS in Bacillus
A;Reference number: S16421; MUID:92216127; PMID:1806041
A;Accession: S16423 RESULT S16423

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 7-286 <GL2>
A;Cross-references: EMBL:X52480; NID:940236; PIDN:CAA36721.1; PID:940239
A;Claser, P.; Kunst, F.; Arnaud, M.; Coudart, M.P.; Gonzales, W.; Hullo, M.F.; Ionesc

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A; Molecule type: DNA
A; Residues: 110-286 < ZUK>
A; Residues: 110-286 < ZUK-
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C;Species: Streptococcus
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A;Title: Nucleotide sequence of the sacS locus of Bacillus subtilis reveals the A;Reference number: JU0293; MUID:90337338; PMID:2116367
A;Accession: PS0148
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A; Residues: 1-286 <KUN>
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A; Residues: 1-286 <GLA>
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                                                                                                                                                                                                           YNETRENPAIVHFCGGEKPWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDIAPYTVAAVED---AGQHERLKEMNVTDTGKYFNSGIMIIDFESWRKQNITEKVINFI 182
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                                                                                                                                                                                                                                                                       -TNTAMPVAVSHYCGSAKPWH
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                                                  SP1766 [imported] - Streptococcus
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glycosyl transferase, family 8 SP1765 [imported] - Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001 C;Accession: 695205 [imported] Spin C;Accession: 695205 [imported] Spin C;Accession: 505205 [i
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A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: H95205
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A; Residues: 1-406 <KUR>
A; Cross-references: GB:AE005672; PIDN:AAK75841.1;
A; Experimental source: strain TIGR4
C; Genetics:
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C:Accession: H95205
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A;Accession: G95205
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A; Res.Jdues: 1-398 <KUR>
A; Cross-references: GB:AE005672; pIDN:AAK75840.1; pID:g14973262;
A; Experimental source: strain TIGR4
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27.5%; Pred. No. 3.4e-13;
7ative 53; Mismatches 127;
14.1%; Score 233; DB 2; 27.5%; Pred. No. 1.1e-12; tive 42; Mismatches 115
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Radune, D.; Holtzappl
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          38;
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IVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEE-----NRAAVAANLRGGGN 57 IVLAADNAYLIPLETTIKSV--LYHNRDVDFYILNSDIAPEWFKLLGRKMEVVN---

-ST 58

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RESULT 5
 iller, L.; Grotbeck, E.J.; Davis, N.W.;
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemory
                                                                              probable LPS biosynthesis enzyme waaI [imported] - Escherichia coli (strain
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H91191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: H91191
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C;Superfamily: lipopolysaccharide glucosyltransferase
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A; Residues: 1-335 <HAY>
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                                                  R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau,
                                                                  C; Accession: A86039
                                                                                                                                    A86039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein ECs4504 [imported] - Escherichia coli (strain 0157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB:BA000007;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MDIVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEENR-----AAVAANLRGG 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLKGYSIGAVDDVYA--YEGRKSG-----FNTGMLLMDVAKWKEHSIVNSLLELAA 165
                                                                                                                                                                                                                                                                                                                                   LDYQFSTNEIAAVV---AERDVEWWQNRASVLTTPQLASG--YFNAGFLLINIDEWNLNN
                                                                                                                                                                                                                                                                                                                                                                                                                                   GNIRFIDVNPEDFAGFPLNIRHISITTYARLKLGEYI-ADCDKVLYLDTDVLVRDGLKPL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPTIVHYASHDKPWN----TYSISRLREL
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                                                                                                                                                                                                    DKVDNPVNDD-----TVFIHYVGPTKPWH 272
                                                                                                                                                                                                                                                                                                                                                                                                    --INIYVINCDKLKSLP-STKNWTYATYFRFTIADYFYHKHEKILYLDADIACKGSIKEL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVAVSHYCGSAKPWHRDCTVWGAERFTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLGGNWVGACIDLFVERQEGYKQKIGMADGEYYFNAGVLLINLKKWRRHDIFKMSCEWVE 177
                                                                                                                                                                                                                                   SRHTDPLYLDRTNTAMPVAVSHYCGSAKPWH 252
                                                                                                                                                                                                                                                                                                                                                                    WDTDLGGNWVGACIDLFVERQ-EGYKQKIG-----MADGEYYFNAGVLLINLKKWRRHD 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDTAFGIDRNFLFGCGVATASILLNNREISCEFHVFTDYISDKDKLYFSDLAKQYNSR--
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                                                                                                                                                                                                                                                                     ISSKAIEMLRDPDWVSK----ITHLDQDVLNVLLNGKVKFISEKYN---TRYSINYE-LK 248
                                                                                                                                                                                                                                                                                                    IFKMSCE-----WVEQYKDVMQYQDQDILNGLFKGGVCYANSRFNFMPTNYAFMANGFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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Masunaga, T.; Kuhara, S.;
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26.9%;
enterohemorrhagic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 220; Db 2
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Shiba, T.; Hattori, M.;
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                                  Lim,
                                  A.; Dimalanta,
Escherichia
                                                  В.;
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                               Glasner,
lanta, E.;
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 0157:H7
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                                  J.D.; Rose, Potamousis,
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S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.;
A;Title: Complete genome sequence of a multiple c
A;Reference number: AB0502; PMID:11677608
A;Accession: AH0972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lipopolysaccharide 3-alpha-galactosyltransferase (EC 2.4.1.44) - C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 2 C;Accession: AH0972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-335 <STO>
A;Cross-references: GB:AE005174; NID:g12518382; PIDN:AAG58773.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A86039
A;Status: preliminary
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C;Superfamily: lipopolysaccharide glucosyltransferase I
C;Keywords: glycosyltransferase; hexosyltransferase
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C;Superfamily: lipopolysaccharide glucosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AL513382; PIDN:CAD03276.1; PID:g16504897; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-337 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
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                                                                                                                                                                                                                                 Query Match
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                                                                                        29 NIAYGIDKNFLFGCGVSIASVLIANREKALAFHVFTDFFGPEDQQRFDALAKQYATQIVV
                                                                                                                                                                                                             LOCAL
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                                                                                                                                    2 DIVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLD--AGISEENRAAVAANLRGGGNIR 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDYQFSTNEIAAVV---AERDVEWWQNRASVLTTPQLASG--YFNAGFLLINIDEWNLNN
YL-IDCERLKSLP-STKNWTYATYFRFIIADYFSDKTDRVLYLDADIACKGSIQELIDLN
                                            FIDVNPEDFAGFPLNIRHISITTYARLKLGEYIAD-CDKVLYLDTDVLVRDGLKPLWDTD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRHTDPLYLDRTNTAMPVAVSHYCGSAKPWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISSKAIEMLRDPDWVSK----ITHLDQDVLNVLLNGKVKFISEKYN---TRYSINYE-LK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IFKMSCE-----WVEQYKDVMQYQDQDILNGLFKGGVCYANSRFNFMPTNYAFMANGFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WDTDLGGNWVGACIDLFVERQ-EGYKQKIG-----MADGEYYFNAGVLLINLKKWRRHD 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --INIYVINCDKLKSLP-STKNWTYATYFRFIIADYFYHKHEKILYLDADIACKGSIKEL
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                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                           12.7%;
25.9%;
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                                                                                                                                                                                     47;
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                                                                                                                                                                                                           Score 210; DB 2;
Pred. No. 9.5e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 220; DB 2;
Pred. No. 1.2e-11
                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    drug resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simmonds, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109;
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                                                                                                                                                                                                                               Length 337;
                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skelton, J
Salmonella
                                                                                                                                                                                  48;
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                                                                                                                                                                                  Gaps
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146
                                                                                          88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enterica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enterica
                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stevens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N.; Farr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
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LGGNWVGACIDLFVERQEG----YKQKI----

-GMADGEYYFNAGVLLINLKKWRRHDI 168

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RESULT 8
C95206
G95206
G95206
G1ycosyl transferase, family 8 Sp1770 [imported] - Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: C95206
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peters
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.;
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
Science 293, 498-506, 2001
                                                                                                                                                                                                                                                                                                  RESULT 9
C42982
                                                                                                                               lipopolysaccharide 3-alpha-galactosyltransferase (EC 2.4.1.44) - Escherichia coli (strai N;Alternate names: lipopolysaccharide core assembly protein rfaI; UDP-D-galactose-(glucc c;Species: Escherichia coli C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 01-Mar-2002 C;Accession: C42982; 847848; E65163 R;Pradel, E.; Parker, C.T.; Schnaitman, C.A. J. Bacteriol. 174, 4736-4745, 1992 J. Bacteriol. 174, 4736-4745, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus A;Reference number: A95000; MUID:21357209; PMID:11463916 A;Accession: C95206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
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A; Contents: K-12
A; Accession: C42982
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-404 < KUR>
                                                                                       A; Title: Structures of the rfaB, rfaI, rfaJ, and rfaS genes A; Reference number: A42982; MUID:92325066; PMID:1624461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: SP1770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEENRAAVAANLRGGG----NI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLYLDRTNTAMPVAVS----HYCGSAKPWHRDCTVWGA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAENEIAAVV-----AEGELEWWTKRSVSLATPGLVSG--YFNAGFILINIPLWTAENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKKAIEMLKDPEVVQRITHLDQDVLNILLVNKARFVDKKFNTQ-----FSLN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKMSCEWVEQYKDVMQ--YQDQDILNGLFKGGVCYANSRFNFMPTNYAFMANGFASRHTD 226
                                                                                                                                                                                                                                                                                                                                                                                                                      DRTNTAMPVAVSHYCGSAKPWHRDCTVWGAERFTEL: | : | : | | | | | | | | | :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEQYKDVMQYQDQDILNGLFKGGVCYANSRFNFMPTNYAFMANGFASRHTDPLY----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGGNWVGACIDLFVERQEGYKQKIGMADGEY---YFNAGVILINLKKWRRHDIFKMSCEW 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIVD---HVLKKFHLPLKNLSYATFFRYFIPNFVKE-SRALYLDSDIIVTGSLDYLFDIE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVFNADNDYVDKLETAIKSI--CCYNNCLKFYVFNDDIASEWELMMNKRLKTIQSEIVNV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --YELKDSVINPVDAETVEVHYIGPTKPWHS----WGA
                                                                                                                                                                                                                                                                                                                                                                                            ELKNGDLP-SVIHYTG-VKPWE----IISNNRFREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNOYHET-AYGDQGILNMLF------HDRWKRLDRNFNFMVGMDSVAHIEGNHKWYEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFIDVNPEDFAGFPLNIRHISITTYARLKLGEYIADCDKVLYLDTDVLVRDGLKPLWDTD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDGYALAAVEDSF------GDVPSTNFNSGMLLVNVDTWRDEDACSKLLEL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         266
                                                                                                                                                                                                                                                                                                                                                                                            246
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Radune, D.; Holtzapple,
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                                                                                                                   coli
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A; Residues: 1-339 <PLUV
A; Cross-references: EMBL:U00039; NID:g466582; PIDN:AAB18604.1; PID:g466765
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;
R; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: E65163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-339 <PRA>
A;Cross-references: GB:M80599; GB:M86935; NID:9146650; PIDN:AAA24086.1; PII
- White amusine extracted from NCBI backbone (NCBIN:108180, NCBIP:108185)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE000440; GB:U00096; NID:g2367252; PIDN:AAC76651.1; A;Experimental source: strain K-12, substrain MG1655 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Start codon: GTG
C;Superfamily: lipopolysaccharide glucosyltransferase
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; nucleic acid sequence not shown; translation A; Molecule type: DNA \,
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302
                                                                                       263
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                                          284 PPTKCMLQRWRKK
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                                                                                                                                                                                                                                                                                                                                                                                      AIAMLNEPEIIKKITHPDQDVLNMLLADKLIFADIKYNTQFSLNYQLKESFINPVTNDTI 262
                                                                                                                                                                                                           SCEWVEQYKDV--MQYQDQDILNGLFKGGVCYANSRFNF-MPTNYAFMANGFASRHTDPL 228
                                                                                                                                                                                                                                                                       FPDDKVAMVV---TEGQADWWEKRAHSLGVAGIAKG--YFNSGFLLINTAQWAAQQVSAR 202
                                                                                                                                                                                                                                                                                            LGGNWVGACIDLFVERQEGYKQK------IGMADGEYYFNAGVLLINLKKWRRHDIFKM 171
                                                                                                                                                                                                                                                                                                                                                                 IYLINGDRLRSLP-STKNWTHAIYFRFVIADYFINKAPKVLYLDADIICOGTIEPLINFS 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDIAYGTDKNFLFGCGISIASILKYNEGSRLCFHIFTDYFGDDDRKYFDALALQYKTRIK
KPNNSNQLRYSAK
                                                                                          FI---
                                                                                                                                  YLDRTNTAMPVAVSHYCGSAKPWHRDCTVWG-----AERFTELAGSLTTVPEEWRGKLAV 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity
67; Conserv
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  314
                                             296
                                                                                       HYIGPTKPWHD----WAWDYPVSQAFMEAKNA---
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21.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 4.5e-09;
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glycosyl transferase homolog T10M13.14 - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_chang C; Accession: T01514 R; Johnson, A.F.; de la Bastide, M.; Lodhi, M.; Hoffman, J.; Ha Martienssen, R.; McCombie, W. submitted to the EMBL Data Library, May 1997 A; Description: The sequence of the Arabidopsis thaliana T10M13 A; Reference number: Z14346 A; Accession: T01514 RESULT 10 T01514 A; Molecule type: DNA A; Residues: 1-346 <J A; Status: translated from GB/EMBL/DDBJ #text_change 24-Mar-1999 Hasegawa, Α.; Gnoj,

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Η.;

Ħ Marzia Tallo

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RESULT 11
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A; Residues: 1-517 <AND>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: The genome sequence of Rickettsia prowazekii and the A;Reference number: A71630; MUID:99039499; PMID:9823893 A;Accession: A71707 A;Status: preliminary; nucleic acid sequence not shown; translability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lipopolysaccharide 1,2-glucosyltransferase (rfaJ) RP476 - Rickettsia prowazekii C;Species: Rickettsia prowazekii C;Species: Rickettsia prowazekii C;Datc: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000 C;Accession: A71705 C;Accession: A71705 R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
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A; Note: T10M13.14
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A;Experimental source: cultivar Columbia
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                                                                                                                                                                              KKWRRHDIFKMSCEWVEQYKDVMQYQDQDILNGLFKGGVCYANSRFNFMPTNYAFMANGF
                                                                                                                                                                                                                                     VLRDLNSLKKIDM-NNYIAACSLDTAITYCIHKVQEECKRNVAHS----YKNSGIVFLNL
                                                                                                                                                                                                                                                                                            VRDGLKPLWDTDLGGNWVGAC-IDLFV-----ERQEGYKQKIGMADGEYYFNAGVLLINL 160
                                                                                                                                                                                                                                                                                                                                                      YIRDYSIDFTTFPDNILNKALTYKEIKFSNNWPSLVMYRLYFDKIFPNLDSILYLDADIV
                                                                                                                                                                                                                                                                                                                                                                                                            FIDVNPEDFAGFPLNIRHISIT------TYARLKLGEYIADCDKVLYLDTDVL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDIALTINDKYAIHAAAVIASSLLNSDLDSFYRFHI----VMDSNDPISQESINKLSSMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MDIVFAADDNYAAY-LCVAAKSVEAAHPDTEIRFHYLDAGISEENRAAVAANLRGGGNIR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FMPTNYAFMANGF-----ASRHTDPLYLDRTNTAMPVAVSHYCGSAKPWHR 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVMVIDLKKWRRGGYTKRIEKWMEIQRRERIYE----LGSLPPFLLVFSGHVAPISHRWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVLLINLKKWRRHDIFKMSCEWVEQYKDVMQYQDQDILNGL-----FKGGVCYANSRFN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDVLVRDGLKPLWDTDLGGNWVGA---CIDLFVERQEGYKQKIGMADGEY------YFNA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---FNIYDFAPETVRGLISSSVRQALEQPLN-----YARSYLADLLEPCVNRVIYLD 172
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                                                             ASRHTDPLYLDRTNTAMPVAVSHYCGSAKPW-----
                                                                                                                    KNMREKQYNNILLETLKNSKCDFSFPDQDLLNVAFQNYLYPLSMRWNFC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGNIRFIDVNPEDFAGF-----PLNIRHISITTYARLKLGEYIADC-DKVLYLD 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GPVSLLHWSGSGKPWIR
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67; Conserv
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TYFEHQSPYFSYFILHY-AEPKPWTTEKEELWKTNHDKLDKITQYYWRYREIT
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ce: strain Madrid E
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26.3%;
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                     A;Molecule type: DNA
A;Residues: 1-572 <SAT>
A;Cross-references: EMBL:AL391143
A;Experimental source: cultivar CC
C;Genetics:
                                                                                                                                                                                                                                                                                     hypothetical protein T20K14_80 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000 C;Accession: T51525 R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tal
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
T51525 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
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C86157
                                                                                                                                                                                                R;Sato, S.; Nakamura, Y.;
submitted to the Protein S
A;Reference number: Z25394
A;Accession: T51525
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A; Map position: 5
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A; Residues: 1-361 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -YARNYLADLLEPCVKRVIYLDSDLVVVDDIVKLWKTGLGQRTIGAPEYCHANFTKYFTG
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Sequence Database,
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27.6%;
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Pred. No. 1.3e-08;
                                                          BAC clone T20K14
                                                                                                                                                                                                                                                          T.; Asamizu,
August 2000
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                                                                                                                                                                                                                                                                                            H.; Tabata,
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RESULT 14
S47847
A;Start codon: GTG
C;Superfamily: lipopolysaccharide glucosyltransferase I
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                       A;Cross-references: GB:AE000440; GB:U00096; NID:g2367252; A;Experimental source: strain K-12, substrain MG1655 R;Pradel, E.; Parker, C.T.; Schnaitman, C.A. J. Bacteriol. 174, 4736-4745, 1992 A;Title: Structures of the rfaB, rfaI, rfaJ, and rfaS gene A;Reference number: A42982; MUID:92325066; PMID:1624461 A;Accession: D42982
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-338 < PLU>
A; Residues: 1-338 < PLU>
A; Cross-references: EMBL:U00039; NID:g466582; PIDN:AAB18603.1; PID:g912479
A; Cross-references: EMBL:U00039; NID:g466582; PIDN:AAB18603.1; PID:g912479
A; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: D65163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lipopolysaccharide glucosyltransferase I (EC 2.4.1.58) - Escherichia coli (strain C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 01-Mar-2002
C;Accession: S47847; D65163; D42982
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A; Note: T20K14_80
                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-338 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: S47666
A; Accession: S47847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Plunkett, G.
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    371 HLRIYIPELFPNLDKVVFLDDDIVVQGDLTPLWDVDLGGKVNGA-----VETCRGEDEWV 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 WLTRENVPVLEAVESHNGVRDYYHGNHVAGANL--TETTPRTFAS-KLQSRSPKYISLLN 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 DNYAAYLCVAAKSVEAAHPDTEIRFHVLD----AG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSHYCGSAKPW 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -ISEENRAAVAA-----HISITT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNILAASVVVSSAVQSSSKPEKIVFHIITDKKTYAGMHSWFALNSVAPAIVEVKGVHQFD
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23.5%;
                                                                                                                                                                                                                                              rfaB, rfaI, rfaJ, and rfaS genes
MUID:92325066; PMID:1624461
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Pred. No. 3.6e-08;
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R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapp nson, T.; Hickey, E.K.; Holt, I.E. science 293, 498-506, 2001
Scienc
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A; Accession: A95206
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Best Local :
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                                                              228 LYLDRTNTAMPVAVSHYCGSAKPWHRDCTVWGAERFTEL 266
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                                                                                                                                                                                                                                                                     CLEEKSLAAVKD----KLKERLIE 158
                                                                                                                                                                                                   Q----YKDVMQYQ-----DQDILNGLFKGGVCYANSRFNFMPTNYAFMANGFASRHTDP 227
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   AFNDK-----PVVI-HFTTYRKPW---
                                                                                                                             QSIVTMKEVEEGREEHFNGDQTIFNQVLQDDWLELGRAYNLQVGHDIVALYNNWQEHL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVLAGDRNYTRQLETTIKSI--LYHNRDVK\\TILNQDIMPDWFRKPRKIARMLGS---EI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADAKLTEKALSILMSKDNVYKYPDQDVMNVLLKGMTLFLPREYN---TIYTIKSELKDKT 248
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Pred. No. 1.4e-
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Pred. No. 4.2e-08;
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Radune, D.; Holtzappl
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                                                                    Pfam; PF01501; Glyco_transf_8; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 330 AA; 39073 MW; C5A6CA0207F24F9A CRC64;
                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                             White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D.; Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
-i- SIMILARITY: TO N. GONORRHOEBE LGTC AND WEAK, TO B.SUBTILIS (LIPOPOLYSACCHARIDE 1,3-GALACTOSYLTRANSFERASE (RFAI) AND TO LIPOPOLYSACCHARIDE 1,2-GLUCOSYLTRANSFERASE (RFAJ).
                                                                                                                                                    EMBL; U32711; AAC21924.1; -. TIGR; HI0258; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=75428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter J.C.;
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NCBI_TaxID=727;
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Bacteria: Proteobacter
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hes 113;
                Similarity
                                                                                                                                    IPR002495; GT_8.
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                32.3%;
                Score 536; DB 1;
Pred. No. 1.1e-40;
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                .1e-40;
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Matches

Conservative

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Mismatches

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P25148;
01-MAY-1992
01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                            Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., M. Presecan E., Santana M., Schneider E., Schweizer J., Ve Rapoport G., Danchin A.; "Bacillus subtilis genome project: cloning and sequenci kb region from 325 degrees to 333 degrees."; Mol. Microbiol. 10:371-384(1993).
                                     the
                                                                                                         CHARACTERIZATION, AND SEQUENCE OF 1-28. MEDLINE=95286551; PubMed=7768864;
                                                                                                                                                                                                  the
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Bacillus subtilis."
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NCBI_TaxID=1423;
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01-FEB-1995 (Rel. 31,
16-OCT-2001 (Rel. 40,
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                                                                                    Antelmann
                                                                                                                                                                        "Nucleotide sequence of the sacs locus the presence of two regulatory genes."; Gene 90:153-155(1990).
                                                                                                                                                                                                                                                              Zukowski M.M., Miller
                                                                                                                                                                                                                                                                                        MEDLINE-90337338;
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RFAI_SALTY STANDARD; PRT; 337 AA.
P19816; 068267;
01-FEB-1991 (Rel. 17, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2014 (Rel. 41, Last annotation update)
Lipopolysaccharide 1,3-galactosyltransferase
RFAI OR WAAI OR STM3718.
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InterPro; IPR002495; GT_8.
Pfam; PF01501; Glyco_transf_8;
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MEDLINE=98204873; pubMed=9535865;
Heinrichs D.E., Monteiro M.A., Perry M.B., Whitfield C.;
Heinrichs D.E., Monteiro the lipopolysaccharide R2 core-type of
"The assembly system for the lipopolysaccharide R2 core-type of
Escherichia coli is a hybrid of those found in Escherichia coli
and Salmonella enterica. Structure and function of the R2 WaaK a
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EMBL; X73124; CAA51568.1; -.
EMBL; M29333; AAA75337.1; -.
EMBL; Z99123; CAB15869.1; -.
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SIMILARITY: TO H.INFLUENZAE HI0259.
SIMILARITY: TO LIPOPOLYSACCHARIDE 1,3-GALACTOSYLTRANSFERASE
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Pred. No. 2.6e-15;
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MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Kyan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
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                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF026386; AAC16412.1; -.
EMBL; AE008873; AAL22577.1; -.
EMBL; X53847; CAA377841.1; ALT_FRAME
PIR; S12097; S12097.
StyGene; SG10337; rfaI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carstenius P., Flock J.-I., Lindberg A.;
"Nucleotide sequence of rfaI and rfaJ genes
lipopolysaccharide glycosyl transferases fro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=LT2
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Pfam; PF01501; Glyco_transf_8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 413:852-856(2001).
[3]
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CATALYTIC ACTIVITY: UDP-galactose + lipopolysaccharide =
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PATHWAY: Lipopolysaccharide core biosynthesis
SIMILARITY: TO E. COLI REAL AND TO REAJ.
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AENEIAAVV-----AEGELEWWTKRSVSLATPGLVSG--YFNAGFILINIPLWTAENIS
                                GGNWVGACIDLFVERQEG-----YKQKI-----GMADGEYYFNAGVLLINLKKWRRHDIF 169
                                                                   YLIDCERLKSLP
                                                                                                                             NIAYGIDKNFLFGCGVSIASVLLANPEKALAFHVFTDFFDSEDQQRFEALAKQYATQIVV
                                                                                                                                                             DIVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVL-DAGISEENRAAVAANLRGGGNIRF
                                                                                             IDVNPEDFAGFPLNIRHISITTYARLKLGEYIAD-CDKVLYLDTDVLVRDGLKPLWDTDL 119
                                                                                                                                                                                                                                                                                                            proteome.
                                                                                                                                                                                                                                                                210
337 AA;
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                                                                                                                                                                                             Conservative
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210 E
38905 MW;
                                                              STKNWTYATYFRFIIADYFSDKTDRVLYLDADIACKGSIQELIDLNF
                                                                                                                                                                                                                                                                                                                             biosynthesis; Glycosyltransferase;
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                                                                                                                                                                                                             13.2%;
26.7%;
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                                                                                                                                                                                            Score 219; DB 1;
Pred. No. 2.9e-12;
5; Mismatches 112
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-> Q (IN REF. 1).
6DB1FA1531AE25F7 CI
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RFAI_ECOLI
                                                                                                        Matches
                                                                                                                      Query Match
Best Local
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MEDLINE=92325066; PubMed=1624461;
Pradel E., Parker C.T., Schnaitman C.A.;
"Structures of the rfab, rfal, rfaJ, and
"Structures of the rfab, rfal, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RFAI_ECOLI
P27128;
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Pfam; PF01501; Glvco +-
Lipopolves--'
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01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lipopolysaccharide 1,3-galactosyltransferase
RFAI OR WAAI OR B3627.
                                                                                                                                                                                                                                                                      EMBL; M80599; AAA24086.1; -. EMBL; U00039; AAB18604.1; -. EMBL; AE000440; AAC76651.1;
                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restricted in the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 22:2576-2586(1994).
-i- CATALYTIC ACTIVITY: UDP-galactose + lipopolysaccharide
galactosyl-lipopolysaccharide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sofia H.J., Burland V., Daniels D.L., Plunkett G. "Analysis of the Escherichia coli genome. V. DNA region from 76.0 to 81.5 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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    Bacteriol.

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KMSCEWVEQYKDVMQ--YQDQDILNGLFKGGVCYANSRFNFMPTNYAFMANGFASRHTDP
                                                                         MDIVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEENRAAV-AANLRGGGNIR
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                                           \verb|LDIAYGTDKNFLFGCGISIASILKYNEGSRLCFHIFTDYFGDDDRKYFDALALQYKTRIK|
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67; Conser
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                                                                                                                     11.5%;
21.4%;
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                                                                                                                     Score 191; DB 1;
Pred. No. 9.4e-10;
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RESULT 5
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ID APAJ_E AC P27129
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RT COLI
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RFAJ_ECOLI STANDADD,
P27129;
01-AUG-1992 (Rel. 23, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FKUM .....

STRAIN=K12 / MG1655;

STRAIN=K12 / MG1655;

MEDLINE=94316500; pubMed=8041620;

Sofia H.J., Burland V., Daniels D.L., Plunkett

*Sofia H.J., Burland V., Daniels D.L., Plunkett

*Analysis of the Escherichia coli genome. V. DN

region from 76.0 to 81.5 minutes. ";

region from 76.0 to 81.5 minutes.";

region from 76.0 to 81.5 minutes.";
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MEDLINE=92355066; PubMed=1624461;
Pradel E., Parker C.T., Schnaitman C.A.;
"Structures of the rfaB, rfaI, rfaI, and rfaS genes of Escherichia"
"Structures of the rfaB, rfaI, rfaI, and rfaS genes of Escherichia"
                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                             EMBL; M80599; AAA24087.1; -. EMBL; U00039; AAB18603.1; -. EMBL; AE000440; AAC76650.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 22:2576-2586(1994).
-i- CATALYTIC ACTIVITY: UDP-glucose + lipopolysaccharide
                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                         Complete proteome.
                                                          InterPro; IPR002495; GT_8.
Pfam; PF01501; Glyco_transf_8; 1.
Lipopolysaccharide biosynthesis; Glycosyltransferase;
                                                                                                                           EcoGene; EG11353;
                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                         glucosyl-lipopolysaccharide.
PATHWAY: Lipopolysaccharide core biosynthesis.
SIMILARITY: TO S.TYPHIMURIUM RFAJ AND TO RFAI.
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                                                                                                                                                                                                                                              an email to license@isb-sib.ch).
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                             McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille I Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heinrichs D.E., Monteiro M.A., Perry M.B., Whitfield C.; "The assembly system for the lipopolysaccharide R2 core-typescharichia coli is a hybrid of those found in Escherichia coli is a hybrid of those found in Escherichia
                                                typhimurium.
Nucleic Acid
                                                                                                                                                                                                     STRAIN-LT2;
                                                                                                                                                                                                                                                                                                                                                                  Ryan E., Sun H., Florea L., Miller W., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Salmonella enterica. Structure and function of the R2 WaaK and WaaL homologs.";
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SEQUENCE OF
                                                                                                                                                       Carstenius P.,
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                                                                                                                         Carstenius P., Flock J.-I., Lindberg A Nucleotide sequence of rfal and rfaJ
                                                                                                                                                                                                                                                                                      Nature 413:852-856(2001).
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                                                   18:6128-6128(1990)
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                                                                                                                                                       Lindberg A.;
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Best Local
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                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
UDP-glucose:glycoprotein glucosyltransferase |
(UDP-Gl::glycoprotein glucosyltransferase) (dl
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EMBL; AE008873; AAL22576.1; -.
EMBL; X53847; CAA37842.1; ALT_FRAME.
PIR; S12098; S12098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brac
                                                                                                          UGT OR UGGG.
                                                                                                                                                                          Q09332;
01-NOV-1997
                                                                                                                                                                                                                    DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002495; GT_8.
Pfam; PF01501; Glyco_transf_8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     StyGene; SG10338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Submitted (JUL-1990) to the
TISSUE=Embryo;
           SEQUENCE
                                    NCBI_TaxID=7227;
                                                   Muscomorpha;
                                                                                                                                                                                                      UGGG_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lipopolysaccharide biosynthesis; Complete proteome.
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PATHWAY: Lipopolysaccharide core biosynthesis
SIMILARITY: TO E.COLI REAJ AND TO REAI.
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336 AA;
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              SEQUENCE
                                                    Drosophilidae;
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Pred. No. 3.8e-08;
6; Mismatches 121
                                                                                                                                                                                                      PRT;
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              OF.
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              23-37
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                                                 Drosophila
                                                                                                                    se precursor (dUGT).
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                                                                 Brachycera;
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Best Local
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                UGGG_SCHPO
Q09140;
16-OCT-2001
16-OCT-2001
15-JUN-2002
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SEQUENCE
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"Drosophila UDP-glucose:glycoprotein glucosyltransferase: seven and characterization of an enzyme that distinguishes between denatured and native proteins.";
EMBO J. 14:1294-1303(1995).
                                                                                                                                                          1413
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal; Transferase; Glycosyltransferase; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0014075; Ugt.
InterPro; IPR002495; GT_8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRS EMBRYOS AND FIRST INSTAR LARVAE BUT IS DETECTED SECOND INSTAR TO PUPATION.
SIMILARITY: SOME, TO YEAST KRE5, S.TYPHIMURIUM RFAJ
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DEVELOPMENTAL STAGE: IS PRESENT AT LOW BUT DETECTABLE LEVELS IN
THE EARLIEST EMBRYOS, INCREASING AT 6-8 HRS WITH A MAXIMUM AT 10-
12 HRS. LEVELS DECREASE THEREAFTER AND ARE NOT DETECTED IN 18-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATHWAY: Glycosylation.
SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                         AAGDRIRGQYQALSQDPNSLSNLDQDLPNNM 1443
                                                                                                                                                                                                                                                                                                               GGNIRFIDVNPEDFAGFPLNIRHISITTYARLKLGEYIADCDKVLYLDTDVLVRDGLKPL
                                                                                                                                                                                    --HDIFKMSCEWVEQYKDVMQYQDQDILNGL 194
                                                                                                                                                                                                                     YDMDLGGAPYAYTPFCDSRKEMEGFRFWKQGYWRSHLM--GRRYHISALYVVDLKRFRKI 1412
                                                                                                                                                                                                                                                 WDTDLGG---NWVGAC----IDLFVERQEGYKQKIGMADGEYYFNAGVLLINLKKWRR- 165
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                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           181
266
864
1545
1548
(Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
:glycoprotein glucosyltransferase precursor (EC 2.4.1.-)
                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                              Score 110.5;
Pred. No. 0.1
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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PREVENT SECRETION FROM ER (
FW; 95D6849961622DB6 CRC64;
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                                                                                                                                                                                                                                                                                                                                               Mismatches
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ER (POTENTIAL).
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UDP-glucose:

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RA Spourcy J., Paat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Raylor K., Simmonds M., Squares R., Squares S., Stevens K.,
RA Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Benito J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Charles M., Schaefer M., Denito J.,
Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
RN Nature 415:871-880(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          absence of the enzyme from Saccharomyces cerevisiae.";
J. Biol. Chem. 269:30701-30706(1994).
-I- FUNCTION: UNFOLDED, DENATURED GLYCOPROTEINS ARE SUBSTANTIALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95074086; PubMed=7982990;
Fernandez F.S., Trombetta S.E., Hellman U., Parodi A.J.;
"Purification to homogeneity of UDP-glucose:glycoprotein
glucosyltransferase from Schizosaccharomyces pombe and apparent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., SEQUENCE OF 19-33 723-730; 983-990 AND 1118-1130, FUNCT COFACTOR, SUBUNIT, AND GLYCOSYLATION. MEDLINE=96181349; PubMed-8631292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., 723-730; 983-990 AN
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                                                                       the European Bioinformatics Institute.
                                                                                                                 between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 19-31,
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                                                                                                                                                                                                                                                                                                                                                                                                                         BIOL. Chem. 269:30701-30706(1994).

BIOL. Chem. 269:30701-30706(1994).

BUNCTION: UNFOLDED, DENATURED GLYCOPROTEINS ARE SUBSTANTIALLY EUNCTION: UNFOLDED, DENATURED GLYCOSYLATION BY THIS ENZYME THAN ARE TO CORRESPONDING NATIVE PROTEINS. THIS PROTEIN AND TRANSIENT GLUCOSYLATION MAY BE INVOLVED IN MONITORING AND/OR ASSISTING FOLDING AND ASSEMBLY OF NEWLY MADE GLYCOPROTEINS, IN ORDER TO FOLDING AND ASSEMBLY OF NEWLY MADE GLYCOPROTEINS, IN ORDER TO THAT NEED ASSISTANCE IN FOLDING FROM
                                                                                                                                                                                                                                                          SUBUNIT: MONOMER.
SUBCELLULAR LOCATION:
                                                                                                                                                                                                                       PTM: GLYCOSYLATED.
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                                                                                                                                                                                                                                                                                                                                                                       COFACTOR: REQUIRES CALCIUM
                                                                                                                                                                                                                                                                                                                                                                                                                 CHAPERONES
                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gwilliam R., Rajandream
                                     non-profit
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                                         institutions as
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ON, SUBCELLULAR
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Best Local
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P50108;
01-OCT-1996
01-OCT-1996
15-JUN-2002
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Glycoprotein.
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CARBOHYD
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                                                                                       SEQUENCE FROM N.A. Dean N., Poster J.
                                                                                                                    Saccharomycetales;
NCBI_TaxID=4932;
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STRAIN=S288c / AB972
                            Submitted
                                               SEQUENCE FROM N.A.
STRAIN-BF264-15DU;
                                                                                                                                        Eukaryota;
                                                                                                                                                   Saccharomyces cerevisiae
                                                                                                                                                             MNN10 OR BED1
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         SEQUENCE FROM N.A
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                                       G.,
                            (JUL-1995)
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                                                                                                                                        ces cerevisiae (Baker's yeast).
Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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(Rel. 41,
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                                                                                                                               Saccharomycetaceae;
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                                                                             Chi J.
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Last annotation update)
MNN10 (EC 2.4.1.-) (Bud
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T -> A (IN REF. 1).
T -> A (IN REF. 1).
D -> H (IN REF. 1).
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0; Mismatches
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Pred. No. 0.
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15-DEC-1998
16-OCT-2001
16-OCT-2001
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CONFLICT
  (Leishmania)
Submitted (N
                                                                                                      Eukaryota; Euglenozoa;
NCBI_TaxID=44271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L42540; AAB48372.1; -. EMBL; U31446; AAC49280.1; -. EMBL; Z49701; CAAB9731.1; -. SGD; S0002653; MNN10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: PUTATIVE GALACTOSYLTRANSFERASE REQUIRED FO
                "Isolation of a gene encoding a DNA topoisomerase II (Leishmania) chagasi.";
                                      Tepe-Lansdell T., Mann B.J., Pearson R.D.,
                                                                 STRAIN=MHOM/BR/86/L669;
                                                                                SEQUENCE FROM N.A.
                                                                                                                                                            DNA topoisomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Golgi stack.
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                                                                                                                                Leishmania chagasi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GROWTH AND EFFICIENT BUDDING.
SUBCELLULAR LOCATION: Type II membrane protein. Golgi
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                           GACSEYSGDSRYFYSEKDHDFVVNMAGCNFGRDC--WGEMQY-----YTTLMEKLNRK
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  .a) chagasi.
(NOV-1999)
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                                                                                                                                                      (Rel. 37, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
merase II (EC 5.99.1.3).
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238
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                                                                                                                    Kinetoplastida; Trypanosomatidae;
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N -> I (IN REF. 2).
                                                   Labombard M.,
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Pred. No. 0.
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                                                                                                                     Leishmania
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RESULT 11
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Matches 64
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                                                                                              1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000616; DNA_topoisoII; ProDom; PD000742; DNA_topoisoIV; SMART; SM00387; HAIPase_c; 1. SMART; SM00433; TOP2c; 1. SMART; SM00434; TOP4c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NP_BIND
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00521; DNA_topoisoIV; 1. Pfam; PF02518; HATPase_C; 1. PRINTS; PR00418; TPI2FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF051307; AAC05295.2; HSSP; P06786; 1BGW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                               1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00204; DNA_gyraseB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00177; TOPOISOMERASE_II; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II MAKES DOUBLE-STRAND BEEAKS.

CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.

SUBUNIT: HOMODIMER (BY SIMILARITY).

SUBUNIT: HOMODIMER (BY SIMILARITY).

SUBCELLULAR LOCATION: Nuclear (BY Similarity).

SUBCELLULAR LOCATION: Nuclear (BY Similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RELAX ONLY NEGATIVE SUPERCOILS. SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC
                                                                                                PVKMW
                                                                                                                                SAKPW
                                                                                                                                                                                                                                                                                                                                                           NEFIAVG--KYTAHPNGRFHISEIPWMTSIEAFRLHISSLASADVVQRIADYSGANHIDI 936
                                                                                                                                                                                                                                                                                                                                                                                         IRFIDVNPEDFAGFPLNIRHIS------ITTYARLKLGEYIADCDKVLYLDT 103
                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt LCNGAVGIGFGFATTIPSFHPLDVSAAVRAMINGESAKQVVRNLVPWAVGFQGTVRRGPD}
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LCVAAKSVEAAHPDTEIRFHVLD-----AGISEENRAAVAANL------RGGGN
                                                                                                                                                               LHKTCVKLGLVRVDESFDYILKKPITF-----
                                                                                                                                                                                             ILNGLFKGGVCYANSRFNFM----PTNYAFMANGFASRHTDPLYLDRTNTAMPVAVSHYCG
                                                                                                                                                                                                                            SDLSPVLQWHYDRRLDLYKRRRTRKIGLMKMDLARLQSTRKFVEHFRQGQIDFLNATDDT
                                                                                                                                                                                                                                                          --LINLKKW---RRHDIFK---------MSCEWVEQYK----DVMQYQDQD 189
                                                                                                                                                                                                                                                                                          DLIVRDGSLTTWAECETDL--------ALAQRI-YINGTVFSPTGTLSPID
                                                                                                                                                                                                                                                                                                                           DVLVRDGLKPLW----DTDLGGNWVGACIDLFVERQEGYKQKIGMADGEYYFNAGVL----
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64; Conser
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1236 AA;
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21.0%;
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75 DNA CLEAVAGE (BY SIMILARITY).
138968 MW; A3209B95A078045C CRC64;
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MEDLINE-91312133; PubMed-1
Schmid K., Ebner R., Jahre
"A sugar-specific porin, S
enteric bacteria.";
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01-AUG-1991
15-JUN-2002
Sucrose pori
SCRY.
                                                                                                                                                                                                                                                                          i.ausport; Sugar transport; Outer membrane; Signal; Plasmid; 3D-structure.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hardesty C., Ferran C., Dirienzo J.m.;
Hardesty C., Ferran C., Dirienzo J.m.;
"Plasmid-mediated sucrose metabolism in Escherichia coli:
characterization of scrY, the structural gene for a
phosphoenolpyruvate-dependent sucrose phosphotransferase
phosphoenolpyruvate-dependent sucrose phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; m38416; AAA98417.1; -. EMBL; X57400; CAA40656.1; -. PIR; S15193; S15193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an modified and this statement is not removed.
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                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003192; Porin_LamB. Pfam; PF02264; LamB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: Porin for sucrose uptake-!- SUBUNIT: HOMOTRIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98100081;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=6153-62;
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                                                                                                                                                                                                                                                                                                                                                                                                ; S15193; S15193.
; A39127; A39127.
; 1A0S; 10-JUN-98.
; 1A0T; 18-MAR-98.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral
                                                                                         AYLCVAAKSVEAAHPDTEI - - - - - RFHYLDAGISE - ENRAAVAANLRGGGNIRF - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Microbiol. 5:941-950(1991).
                                           AMLIALLTSAASAHAQTDISTIEARLNALEKRLQEAENRAQTAENRAGAAEKKVQQLTAQ
                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an email to license@isb-sib.ch).
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(Rel. 19, Last seq
(Rel. 41, Last ann
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e porin.";
173:449-456(1991).
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19.3%;
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IDVNPEDFAGFPLNIRHISITTYARLKLGEYIADCDKVLYLDT 103
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annotation update)
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SCrY
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Best Local :
                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., ReLch C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y635_METJA
Q58052;
                                                                                                                                                                                                                                             Hypothetical protein; Complete proteome. SEQUENCE 283 AA; 32502 MW; 1CE52FC8457C5E20 CRC64;
                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinf
the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Meth
Methanocaldococcaceae; Methanocaldococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                  TIGR;
                                                                                                                                                                                                                                                                                               EMBL; U67511;
                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                            entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
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163
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                                                                                                                                                     NYAAYLCVAAKSVEAAHPDTEIRFHVLDA----GISEENRAAVAAN------LRGGGNIRF
                           IADCDKVLYLDTDVLVRD-GLKPLWD---TDLGGNWVGACI-DLFVERQEGYKQKIGMAD 146
                                                           VIIIEGDYDFDKFKNHLKEIGVNPVEEYGGFKIYTKPNDDKIALTFYKDMIIAGTKQGVY
                                                                                                                      DYNGFYYVNFKNIEDSKYSSEYRSKILNALRLGNANGEKTGIYINKTKRMIFSGSGYDRF
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--DCINVINGEMDSLLKNREVMEIYDRLPSD---
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                                                                                                                                                                                                                                                                                 мJ0635;
                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   273:1058-1073(1996).
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(Rel.
(Rel.
                                                                                                                                                                                       Conservative
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35, Last sequence update)
40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                           license agreement (See http://www.isb-sib.
                                                                                                                                                                                                    5.3%;
                                                                                        ---IDVNP-EDFAGFPL---
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Pred.
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ACVYEVSGTYSPWYKT --
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L outstation -
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Db Qy

211

GMSISFENNDRVKVVRVEKYKDEETAK ----EKYEELLKKKDRD

-EYYFNAGVLLINLKKWRRHDIFKMSCEWVEQYKDVMQYQDQD

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-!- FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY

-!- BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH

THE INFRACELLULAR RETICULATE BODY MEMBRANE.

-!- SUBUNIT: DISULFIDE BOND INTERACTIONS WITHIN AND BETWEEN MOMP

MOLECULES & OTHER COMPONENTS FORM HIGH MOLECULAR-WEIGHT OLIGOMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHLTR
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                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01308; Chlamydia_OMP; 1.
PRINTS; PR01334; CHLAMIDIAOMP;
ProDom; PD001717; Chlamydia_OMP; 1.
Outer_membrane; Transmembrane; Porin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S11010; MMCWTB.
InterPro; IPR000604; Chlamydia_OMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M17342; -; NOT_ANNOTATED_CDS. EMBL; AF304856; AAG41414.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia trachomatis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-B/Tw-5/OT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=87307955; PubMed=3040664;
Stephens R.S., Sanchez-Pescador R., Wagar
"Diversity of Chlamydia trachomatis major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=87307955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OMPA OR OMP1B
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01-NOV-1991
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150 YFNAGVLLINLKKWRRHDIFKMSCEWVEQYKDVMQYQDQDILNGLFKGGVC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence analysis of the major outer membrane protein gene
                                                         65
                                                                                                       92
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                                                                                                                                                                                                              48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriol. 169:3879-3885(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute.
                                                YGDFVFDRVLKTDVNKEFQMGAKP---TTTTGNAV-APSTLTARENPAYGRH--MQDAEM 118
                                                                                                                                                                                                            VAANLRGGGNIRFIDV-NP------EDFAGFPLNIRHISITTYA---RLKLGEY 91
                                                                                                    IAD--CDKVLYLDTDVLVRDGLKPLWDTDLGGNWVGACIDLFVERQEGYKQKIGMADGEY 149
                                                                                                                                                        VFAALSSASSLQALPVGNPAEPSLMIDGILWEGFGGDPCD----PCTTWVDAISMRMG-Y 64
                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and this statement is not removed. requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                       394 AA;
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                                                                                                                                                                                                                                                          26; Mismatches
                                                                                                                                                                                                                                                                                           Score 87; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                             MAJOR OUTER MEMBRANE PROTEIN,
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                                                                                                                                                                                                                                                                                                                                                                       C364233145A69301 CRC64;
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                                                                                                                                                                                                                                                                                                                   DB 1;
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outer
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                                                                                                                                                                                                                                                                                                              Length 394;
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DPOM_ASCIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1991 (Rel. 19, Create 01-AUG-1991 (Rel. 19, Last s 15-DEC-1998 (Rel. 37, Last a Probable DNA polymerase (EC
 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              extrachromosomal DNA of the ascomycete Ascobolus immersus."; Mol. Gen. Genet. 218:523-530(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPOM_ASCIM P22374;
                                                                                                                                                                                                                                                 PROSITE; PS00116; DNA_POLYMERASE_B; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
DNA-binding; Plasmid; Mitochondrion.
SEQUENCE 1202 AA; 138279 MW; 51D41FCEBDBF2CDE CRC64;
                                                                                                                                                                                                                                                                                                               Pfam; PF03175; DNA_pol_B_2; 1. SMART; SM00486; POLBC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=2/I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Pezizomycotina; Pezizomycetes;
Pezizales; Ascobolaceae; Ascobolus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pAI2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ascobolus immersus.
                                                                                                                                                                                                                                                                                                                                             InterPro; IPR004868; DNA_pol_B_2.
                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002064; DNA_pol_B
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X15982; CAA34106.1; -.

    -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "In organello replication and viral affinity of linear,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kempken F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=5191;
                                                                                                                          967
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                                                                                             86
                                                                                                                                                         31
                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISCELLANEOUS: THIS DNA POLYMERASE REQUIRES A PROTEIN AS A PRIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA POLYMERASE OF OTHER FUNGAL AND PLANTS MITOCHONDRIAL PLASMIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                               S05362;
MKHEYTFKEAVFVAPKVYGGLFDKPYKNKVETVK-----VKGLKEPIQYSD
                             ADGEYYFNAGVL-----LINLKKWRRHDIFKMSCEWVEQYKDVMQYQD
                                                                                         LKLGEY-IADCDKVLYLDTDVLVRDGLKPLWDTDLGGNWVGACIDLFVERQEGYKQKIGM 144
                                                                                                                          IXYSVLTPEESEEKLKNSSCIEATTLPSGNVLFKENKPLGEFSNLNTSVPISAAIAAYSR 1026
                                                                                                                                                       IRFHVLDAGISEE----NRAAVAANLRGGGNIRFIDVNP-EDFAGFPLNIR-HISITTYAR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTNAACMALNI - - WDRFDVF - - - C - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNENQTKVSNGAFVPNMSLDQSVVELY---TDTAFAWSVG---ARAALWECGCATLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSRFNFMPTNYAFMANGFASRHTDPLYLDRTNTAMPVAVSHYCGSAKPWHRDCTVWGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (N)
                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Meinhardt F.,
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                               S05362.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=2573821;
ardt F., Esser K.;
                                                                                                                                                                                                     5.2%;
22.8%;
                                                                                                                                                                                      32;
                                                                                                                                                                                                   Pred.
                                                                                                                                                                                                     Score 86.5;
Pred. No. 1
                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                      61;
                                                                                                                                                                                                                    1;
                                                            -VDTEIDKKYVSDKELGL 1066
                                                                                                                                                                                                                  Length 1202;
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EMBL; AF040747; AAC09268.1; -.
EMBL; AF040748; AAC09269.1; -.
EMBL; AF040749; AAC09270.1; -.
EMBL; Y17967; CAA76975.1; -.
EMBL; Y17967; CAA75789.1; -.
EMBL; Y15798; CAA75789.1; -.
EMBL; Y15799; CAA75790.1; -.
HSSP; Q63450; 1A06.
     PRINTS: PROO717; GPORKINASE.

PRODOM; PD000001; Euk_pkinase; 1.

SMART; SM001315; RGS; 1.

SMART; SM00133; S_TK_X; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRK6_MOUSE STANDARD; PRT; 576 ÅA.

070293; 070294;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16 protein-coupled receptor kinase GRK6 (EC 2.7.1.-) (G-protein-coupled
                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:1347078; Gprk6.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000239; GPCR_kinase.
InterPro; IPR000961; Pkinase_C.
InterPro; IPR000342; Regl_Gprotein.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long of modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: SPECIFICALLY PHOSPHORYLATES THE ACTIVATED |
PROTEIN-COUPLED RECEPTORS (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Membrane-bound.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; GRK6A (SHOWN HERE)
ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=129/SvJ, and C57BL/6J; TISSUE=Thymus; Moepps B., Vatter P., Frode R., Waechter F., Gierschik P.; "Primary structure of murine G-protein-coupled receptor ki splice variants predict differential regulation by posttra modifications.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Premont R.T., Lefkowitz R.J.;

"Genomic organization of the GRK5 and GRK6 genes:
among the GRK4 subfamily of g protein-coupled rece
evolution of the GRK gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor kinase 6). GPRK6 OR GRK6.
Phosphorylation; Lipoprotein; DOMAIN 1 185
                                                                                                                                                                                                                                                                                                                              Pfam; PF00069; pkinase; 1. Pfam; PF00615; RGS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the ENEUROPEAN BLOODEAN THE THE BUTOPEAN BLOODEAN BLOODE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (JAN-1998) to the EMBL/GenBank/DDBJ databases
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N-TERMINAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Usage
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Murinae; Mus
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                                                                                                                                                                            FYAAEICCGLEDLHRERIVYRDLKPENILLDDHGHIRISDLG-----LAVHVPEGQTI 342
                                                                                                                                                                                                EYIAD-CDKVLYLDTDVLVRDGLKP---LWD-----TDLGGNWVGACIDLFVERQEGY 138
                                                                                                                                                                                                                        RF-VVSLAYAYETKDALCLVLTLMNGGDLKF------HIYHMGQAGFPEARAV
FQELNVFGLDGSVPPDLDWKGQPTAPPKKGLLQR
                    FTEL--AGSLTTVPE--EWRGKLAVPPTKCMLQR 292
                                                                 ----ASRHTDPLYLDRTNTAM-----PVAVSHY----CGSAK-PWHRDCTVWGAER
                                                                                      EVAEEYTDRFSSQARSLCSQLLSKDPAERLGCRGGGAREVKEHPLFKKLNFKRLGAGMLE
                                                                                                          EWVEQYKDVMQYQDQDILNGLFK----
                                                                                                                                 KGRVGTVGYMAPEVVRNERYTFSPDWWALGCLLYEMIAGQSPFQQRKKKIKREEVERLVK 402
                                                                                                                                                       KQKIG------MADGEYYFN----AGVLLINL------
                                           PPFKPDPQAIYCKDVLDIEQFSTVKGVDLEPTDQDFYQKFATGSVSIPWQNEMV--ETEC
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                                                                                                                                                                                                                                                                            5.1%;
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                                                                                                                                                                                                                                                                             Score 85;
Pred. No.
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QAEAPTGGWR (IN ISOFORM GRK6B).
                                                                                                                                                                                                                                                                                                                                              PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                               C-TERMINAL.
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PHOSPHORYLATION (AUTO-)
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ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                    Mismatches
                                                                                                            GGVCYANSRENEMPTNYAFMANGE --
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                                                                                                                                                                                                                                                                   121;
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SIMILARITY).
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arch completed: December 2, 2002, 11:56:27 b time: 8.44739 secs

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  1631.5
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Copyright (c) 1993 - 2002 Compugen Ltd
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09c1s0 pasteurella
09rex6 neisseria g
09rgn0 neisseria g
0917a2 haemophilus
09ahb5 streptococc
048480 klebsiella
08vu29 streptococc
097p76 streptococc
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Q9rex5 neisseria g
P96945 neisseria m
Q93ek7 neisseria m
Q93eb2 pasteurella
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Q8Z2G2	Q9M8J2	Q92VQ2	Q9AEU2	Q8VYF4	Q9LZJ9	Q97P72	Q8XDC2	Q9ZNA6	Q97P75	Q9MAB8	Q9LF35	Q9FWY9	068204	068205	Q9ZD68	004253	Q9ZIS6	Q9R9D2	Q52832	Q97P73	Q8Z2G3	Q9ZIS8	Q9ZIS5	Q9R9D1	Q9ZIS1	Q48484	Q93RH6	Q8XDC0
Q8z2g2 salmonella		2	٠,		Q9lzj9 arabidopsis		2	Q9zna6 erythrobact				9	068204 escherichia	068205 escherichia		004253 arabidopsis	Q9zis6 escherichia	Q9r9d2 escherichia	')	Q97p73 streptococc	Q8z2g3 salmonella	Q9zis8 escherichia	Q9zis5 escherichia	_	•		Q93rh6 streptococc	Q8xdc0 escherichia

ALIGNMENTS

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Db 61 IDVNPEDFAGFPLNIRHISITTYARLKLGEYIADCDKVLYLDTDVLVRDGLKPLWDTDLG 120	QY 61 IDVNPEDFAGFPLNIRHISITTYARLKLGEYIADCDKVLYLDTDVLVRDGLKPLWDTDLG 120	Db 1 MDIVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEENRAAVAANLRGGGNIRF 60	Qy 1 MDIVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEENRAAVAANLRGGGNIRF 60	Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps	SQ SEQUENCE 306 AA; 34857 MW; 178B5208FD88AACB CRC64;	KW Transferase.	DR Pfam; PF01501; Glyco_transf_8; 1.	DR Interpro; IPR002495; GT_8.	Neisseria gonorrhoeae lipooligosaccharide.";		RX MEDLINE=95053752; PubMed=7964493;		OX NCBI TaxID-485;	Neisseria gonorrhoeae.	LGTC.	01-MAR-2002 (TrEMBLrel. 20,	01-NOV-1996 (TrEMBLIEL 01.	01-NOV-1996 (TrEMBLrel.	050948;	ID 050948 PRELIMINARY: PRT: 306 AA.	RESULT 1	
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"Mutations in the 1gt operon inf

gonococci.";

Submitted (NOV-1999) to the EMBL

EMBL; AF208062; AAF20991.1; -

InterPro; IPR002495; GT_8.

Pfam; PF01501; G1yco_transf_8; 1

SEQUENCE 307 AA; 34903 MW; 0
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01-MAY-1997 (TrEMBLrel. (
01-MAY-2002 (TrEMBLrel. ;
Glycosyl transferase.
LGTC.
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01-DEC-2001
01-DEC-2001
01-MAR-2002
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LGTC.
Neisseria |
Bacteria;
Zhu P., Klutch M.J., Tsai C.M.; "Genetic Analysis of Conservation and Variation of Lipooligosaccharide Expression in Two L8-Immunotype Strains of Neisseria meningitidis."; FEMS Microbiol Lett. 203:173-177(2001).
                                                                            MEDLINE=21467954; PubMed=11583844; Zhu P., Klutch M.J., Tsai C.-M.:
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SEQUENCE
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Bacteria; Proteobacter
NCBI_TaxID=487;
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                                                                                                                       STRAIN=M978
                                                                                                                                                                                 NCBI_TaxID=487;
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"Identification of Pasteurella multocida virulence genes in
"Experiment mouse model using signature-tagged mutagenesis.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF237927; AAF68413.1; -.
InterPro; IPR002495; GT_8.
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Pfam; PF01501; Glyco_transf_8;
SEQUENCE 311 AA; 35738 MW;
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                     LGGNWVGACIDLEVERQEG-YKQKIGMADGEYYFNAGVLLINLKKWRRHDIFKMSCEWVE 177
                                                                                                                   FIDVNPEDFAGFPLNIRHISITTYARLKLGEYIAD-CDKVLYLDTDVLVRDGLKPLWDTD 118
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                                                                                                                                                                                                                                                                                                Score 572; DB 2;
Pred. No. 1.4e-43;
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Pred. No. 4.2e-132;
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Q9CLS0;
01-JUN-2001
01-JUN-2001
01-MAR-2002
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EMBL; AE006155; AAK03223.1; -.

InterPro; IPR002495; GT_8.

Pfam; PF01501; Glyco_transf_8; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 302 AA; 35716 MW; 6C7264ED8F033C00 CRC64;
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Bacteria; Proteobacteria;
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May B.J., Zhang Q., Li L.L., Paust
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                                                                      RIRYKFKYQVY
                                                                                             KLSARFLRKIY 306
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1 (TrEMBLrel. 17, 1
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al protein PM1139.
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1; Mismatches
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Q9REX6;

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RESULT
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ID Q5
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                   Q9L7A2
Q9L7A2;
Q1-OCT-2000
Q1-OCT-2000
Q1-MAR-2002
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01-MAY-2000
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Bacteria;
                                                                                                                                                                                                                       MEDLINE=20305049; PubMed=10844691; Harvey H.A., Porat N., Campbell C.A., Phillips N.J., Apicella M.A., Balke M "Gonococcal lipooligosaccharide is a receptor on human sperm.";
           Putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002495; GT_8.
Pfam; PF01501; Glyco_transf_8; 1.
SEQUENCE 57 AA; 5934 MW; 392247E1A7C1135D CRC64;
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Balthazar J.T.,
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Proteobacteria;
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Q9AHB5;
Q1-JUN-2001
Q1-JUN-2001
Q1-JUN-2002
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Submitted
                                                         Griffiths D.B., Hall L.M.C.;
"The Cps locus of Streptococcus
cpsE and cpsL.";
                                                                                                                         Jiang S.M., Wang L., Reeves P.R.;
"Molecular characterization of Streptococcus
and 18C capsular polysaccharide gene clusters
Infect. Immun. 69:1244-1255(2001).
                                                                                                                                                                                                                  Streptococcus pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang J., Hanson E., Munson R.S. Jr.;
"Putative glycosyl transferase.";
Submitted (JAN-2000) to the EMBL/Gen:
EMBL; AF224467; AAF28363.1;
InterPro; IPR002495; GT_8.
                  SEQUENCE FROM N.A. STRAIN=SSISP 6A/1;
                                                                                           SEQUENCE FROM N.A. STRAIN=PN93/1413;
                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=21116929; PubMed=11179285;
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WCIN OR CPSP OR CPS6AP.
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Pfam; PF01501;
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NCBI_TaxID=730;
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Bacteria; Proteobacteria;
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(TrEMBLrel. 21, Last annotation update)
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Griffiths "The Capsu

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Q1-NOV-1996;
Q1-MAR-2002
                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-SEROTYDE 08;
MEDLINE-66359375; PubMed-8752339;
MEDLINE-06359375; PubMed-8752339;
MEDLINE-66359375; PubMed-8752339;
MEDLINE-66359375; PubMed-8752339;
MEDLINE-6639375; PubMed-8752339;
MEDLINE-663939;
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                                  SEQUENCE FROM N.A. STRAIN=SEROTYPE 08; MEDLINE=97158136; P
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Q8VU29;
Q1-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF(
SEQUENCE
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EMBL; L41518; AAC98407.1; -. InterPro; IPR002495; GT_8.
                                                                                                                                                                                                                                                                                                                                                            Streptococcaceae;
NCBI_TaxID=1313;
                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                "The Capsular
Serotype 6B.";
                                                                                                                                                                                                                                                                                                            Griffiths D.B.,
                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus
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                                                                                                                                                                                                                                                                                                                           STRAIN=361
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                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium
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DLGGNWVGACIDLFVERQEGYKQKIGMADGEYYFNAGVLLINLKKWRRHDIFKMSCEWVE
                                         NWIE-NVE--IPFKLHLDRGSISSFSRLFLGSVLPSSMSKVLYLDSDIIVMDSLRSILDI
                                                                  RFIDVNPEDFAGFPLNIRHISITTYARLKLGEYI-ADCDKVLYLDTDVLVRDGLKPLWDT 117
                                                                                                                    MDIVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEENRAAV--AANLRGGGNI
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                                                                                            MDIVYATDNNFVDVLSASIKSLYTTNSDLDLNLWIIADKVSDRNKEKINRLSKQFAQREI
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NCE 630 AA; 72599 MW;
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79; Conserv
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27.6%;
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Last sequence
Last annotation
                                                                                                                                              Score 243; DB
Pred. No. 8.9e
63; Mismatches
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Pred. No. 1.9e
47; Mismatches
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hes 117;
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..9e-14;
les 108;
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Q97P76;
Q1-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002495; GT_8.

Pfam; PF01501; Glyco_transf_8; 1.

Transferase; Complete proteome.

SEQUENCE 406 AA; 47412 MW; D1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2001 (TrEMBLrel. 18, I
01-MAR-2002 (TrEMBLrel. 20, I
Glycosyl transferase, family
SP1766.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 293:498-506(2001).
EMBL; AE007469; AAK75841.1; -.
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                  225
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                 ILHYISQDKPWNQFSVGRLREVWWEYSLMD---
                                             VSHYCGSAKPWH-----RDCTVWGAERFTELAGSLTTVPEEWRGKLAVPPTKCML 290
                                                                                                    DVMQYQDQDILNGLFKGGVCYANSRFNFMPTNYAFMANGFASRHTDPLYLDRTNTAMPVA 240
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                                                                                 ENVEEGDQSILNMLFKDQYSSLEDQYNFQ-IGYDYGAATFKHQFIFDIPLE----PLPL-
                                                                                                                                                  ENYLAAARSCF-----
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                                                                                                                                                                                                                                                                                                                                                  81;
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27.5%; Pred. No. 2.96 --
17; Mismatches 127;
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18, Last sequence up
20, Last annotation
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Pfam; PF01501; Glyco_transf_8; 1.
Transferase; Complete proteome.
SEQUENCE 398 AA; 46365 MW; 44
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Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
    Bacteria;
                                                                                WAAS.
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NCBI_TaxID=1313;
                                            Escherichia
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EMBL; AE007469; AAK75840.1; -.
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gamma subdivision; Enterobacteriaceae;
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EMBL; AF019375; AAC69655.1; -.
InterPro; IPR002495; GT_8.
Pfam; PF01501; Glyco_transf_8; 1.
SEQUENCE 290 AA; 33801 MW; 3AlA6FAF40C7AF7B CRC64;
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Heinrichs D.E., Yethon J.A., Whitfield C.;
"Molecular basis for structural diversity in the core regions of the 
"popolysaccharides of escherichia coli and salmonella enterica.";
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Copyright (c) 1993 - 2002 Compugen Ltd
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      AAR91314
AAW06579
AAR91311
AAW06576
AAU72923
AAW89332
AAW89333
AAW89333
AAW893151
AAB47426
AAG90151
                                                                                                                                                                                                                                                                                                           SUMMARIES
N. gonorrhoeae gly
Lipo-oligosacchari
N. gonorrhoeae gly
Neisseria polyglyc
Neisseria polyglyc
Neisseria gonorrhe
Putative glycosylt
EpsN. Lactococcus
C glutamicum prote
Enzyme EPS8 which
                                                                                                                                                                                                                                           Description
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Streptococcus poly	ABP25821	23	310	9.6	169
Lactocc	~ 1	22	N	9.8	173.5
sequen	AAY68985	21	0		174
ive gly	96	22	S	•	175.5
no acid	4	21	N	٠	180.5
e EPS7 whic	4	21	N	٠	180.5
erase	m	20	S.	10.3	181
ດາ	ABB54192	23	4	٠	182
eptococcus	~1	23	-	•	182.5
2J protein	AAY68962	21	w	•	185.5
	4	23	œ	•	185.5
eptococcus pne	AAW61236	19	æ	•	185.5
obacte	~ 1	21	7	•	185.5
acid s	(4)	21	w	•	186.5
nvol		21	ω	•	186.5
obacter	AAY97206	21	0	10.6	187
protein	AAY68,974	21	N	•	187.5
	AAY68975	21	N	•	190
ococcus	ABP26805	23	N	•	194
glutamicum p	AAG90140	22	4	٠	195
treptococcus p	AAY81720	21	N	•	199
S.thermophilus exo	AAW22177	18	N	•	199
.thermo	AAW14078	18	N	•	199
Listeria monocytog	ABB48565	23	N	•	200.5
multocida		21	0	•	201.5
pr	3	21	ω		204
acid s	4	21	σ		205.5
	4	21	g	•	205.5
steurella		23	g	•	207.5
Ħ	33	21	7		207.5
multocio	43	21	7		209
la		20	7		\circ
as	47	23	S		\circ
lto	96	21	965	11.8	209
Amino acid sequenc	7	21	\vdash		-

ALIGNMENTS

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RESULT 1
AAR91314
ID AAR9
  Nucleic acids encoding diagnosis of infection oligo:saccharide(s)
                                   WPI; 1996-200924/20
N-PSDB; AAT14061.
                                                              Gotschlich
                                                                                                                                   04-APR-1996
                                                                                                                                                                     Neisseria gonorrhoeae strain F62
                                                                                                                                                                                               Glycosyltransferase; lipo-oligosaccharide;
                                                                                                                                                                                                               N. gonorrhoeae glycosyltransferase LgtD
                                                                                                                                                                                                                                   09-JUL-1996
                                                                                                                                                                                                                                                    AAR91314;
                                                                                                                                                                                                                                                                     AAR91314 standard; Protein; 337 AA
                                                                                                 26-SEP-1994;
                                                                                                                 25-SEP-1995;
                                                                                                                                                    WO9610086-A1.
                                                                              (UYRQ ) UNIV ROCKEFELLER.
                                                              띥
                                                                                                                                                                                                                                  (first entry)
                                                                                                94US-0312387
                                                                                                                 95WO-US12317.
         glycosyl transferase(s) with Neisseria and for the
                                                                                                                                                                                               lgt gene; LOS
         used in the biosynthesis
                                                                                                                                                                                               locus;
          of
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RRESULT 2
AAWOGS AWO
XX AAWO
XX AAWO
XX Lipo
XX Lipo
XX Poly
KW Poly
KW N-ac
XX W-ac
XX WO96
XX O7-J
XX WO96
X
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Best Local S
Matches 337
                                                                                                                               07-JUN-1995;
                                                                                                                                                                                03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lipo-oligosaccharide gene-encoded protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW06579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contg. activated GalNAC or GicNAC to an acceptor moiety comprising a Gal residue in the presence of LgtD. Oligosaccharides can be produced that, when attached to non-toxic lipids, are useful for Neisseria vacche prepn. Blood group core oligosaccharides, and mimics of lacto-N-neotetraose, gangliosides and saccharide portions of globoglycolipids can also be produced using the enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 Glycosyltransferases (AAR91311-15) are products of the lgt locus (AAT14061) of Neiserria gonorrhoeae strain F62. Glycosyltransferase LgtD (AAR91314) can be obtd. by expression of the lgtD coding sequence in recombinant host cells. A method for adding GalNAc or GlcNAc betal-3 to Gal comprises contacting a reaction mixture
                                                                            (NEOS-) NEOSE
                                                                                                                                                                                                                                    19-DEC-1996
                                                                                                                                                                                                                                                                                       WO9640971-A1
                                                                                                                                                                                                                                                                                                                                        Neisseria gonorrhoeae ATCC 33084
                                                                                                                                                                                                                                                                                                                                                                                            N-acetylgalactosaminyl transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                     Polyglycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLRFDPAYIHAEDYKFWYEAGKLGRLAYYPEALVKYRFHQDQTSSKYNLQQRRTAWKIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MQPLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGRI 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGAWLEVLSEENNKSVLAAIARNGAIWDKPTRHEDIVAVFPFGNPIHNNTMIMRRSVIDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLRFDPAYIHAEDYKFWYEAGKLGRLAYYPEALVKYRFHQDQTSSKYNLQQRRTAWKIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al Similarity
337; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                        Johnson KF,
                                                                            TECHNOLOGIES INC
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                                                                                                                               95US-0478140
                                                                                                                                                                                96WO-US08323.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                               N-acetylglucosaminyl transferase;
                        Roth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Pred. No. 3.6e-178;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                         lipo-oligosaccharide
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RESULT 3
AAR91311
ID AAR9
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                       Glycosyltransferase;
                                                                                                                                                                                                                                                                          AAR91311 standard;
                                                                                                                                 Neisseria gonorrhoeae strain
                                                                                                                                                                                                                        09-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stated in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gonorrhoeae ATCC 33084 includes coding sequences for 5 proteins (AAW06576-80), one of which (AAW06576) is a polyglycosyltransferase that catalyses the addition of GloNAc and GalNAc disachbarides to a galactose moiety. The function of the other 4 proteins is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 2E-F; 38pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transfer of at least 2 saccharide units using poly:glycosyl:transferase - isolated from N. gonorrhoeae, catalyses the addition of both GlcNac and GalNac di:saccharide(s) units to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-052351/05
N-PSDB; AAT49230.
         (UYRQ ) UNIV
                                 26-SEP-1994;
                                                          25-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                              gonorrhoeae glycosyltransferase LgtA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDLLDFLTDRVMRKLFAAPQYRKILKKMLRPWKYRSY
                                                                                                                                                                                                                                                                                                                                                                                      EIRAGYWKAAGIAVGADCLNYGLLKSTAYALYEKALSGQDIGCLRLFLYEYFLSLEKYSL
                                                                                                                                                                                                                                                                                                                                                                                                                EIRAGYWKAAGIAVGADCLNYGLLKSTAYALYEKALSGQDIGCLRLFLYEYFLSLEKYSL
                                                                                                                                                                                                                                                                                                                                                                                                                                        GLRFDPAYIHAEDYKFWYEAGKLGRLAYYPEALVKYRFHQDQTSSKYNLQQRRTAWKIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGAWLEVLSEENNKSVLAAIARNGAIWDKPTRHEDIVAVFPFGNPIHNNTMIMRRSVIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336;
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           ROCKEFELLER
                                                                                                                                                                                                                        (first entry)
                                 94US-0312387
                                                          95WO-US12317
                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.8%;
99.7%;
                                                                                                                                                                       lipo-oligosaccharide;
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                                                                                                                                                                                                                                                                           348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1761; DB 18;
Pred. No. 7.5e-178;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene region (AAT49230)
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                                                                                                                                                                       lgt gene;
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                                                                                                                                                                       SOT
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                                                                                                                                                                       locus;
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                                                                                                                                                                                                                                                                                        밁
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria vaccine prepn. Blood group core oligosaccharides, and mimics of lacto-N-neotetraose, gangliosides and saccharide portions of globoglycolipids can also be produced using the enzymes.
                                                                 Neisseria
                                                                                           N-acetylgalactosaminyl transferase;
                                                                                                        Polyglycosyltransferase; N-acetylglucosaminyl transferase;
                                                                                                                                   Neisseria polyglycosyltransferase
                                                                                                                                                                21-MAR-1997
                                                                                                                                                                                          AAW06576;
                                                                                                                                                                                                                     AAW06576 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 Glycosyltransferases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oligo:saccharide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding diagnosis of infection
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                                        WO9640971-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AAT14061) of Neiserria gonorrhoeae strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MQPLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGRI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1996-200924/20
DB; AAT14061.
                                                                                                                                                                                                                                                                                                                                                           KEEIRAGYWKAAGIAVGADCLNYGLLKSTAYALYEKALSGQDIGCLRLFLYEYFLSLEKY 298
                                                                                                                                                                                                                                                                                                                                                                                                                  DGGLRFDPAYIHAEDYKFWYEAGKLGRLAYYPEALVKYRFHQDQTSSKYNLQQRRTAWKI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSGAWLDFAADGRMRRLFTLRQYFGILYRLIK 332
                                                                                                                                                                                                                                                                                                               SLTDLLDFLTDRVMRKLFAAPQYRKILKKMLR 330
                                                                                                                                                                                                                                                                                                                                            QKTARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEKDLPEEDFERARRFLYQCFKRTDTP 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       IAMGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNPIHNNTMIMRRSVI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAMGAWLEVLSEENNKSVLAAIARNGAIWDKPTRHEDIVAVFPFGNPIHNNTMIMRRSVI 178
                                                                gonorrhoeae
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                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.5%;
                                                                   ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AAR91311-15) are products of the lgt locus a gonorrhoeae strain F62. Glycosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycosyl transferase(s) - used in the with Neisseria and for the biosynthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33;
                                                                   33084
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Pred. No. 2.5e-102;
3; Mismatches 83;
                                                                                           lipo-oligosaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 348;
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RESULT 5
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Best Local S
Matches 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gonorrhoèae ATCC 33084 catalyses the stereospecific conjugation of 2 specific activated saccharide units (e.g. UDP-GLNAC, UDP-GALNAC, UDP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transfer of at least 2 saccharide units using poly:glycosyl:transferase - isolated from N. gonorrhoeae, catalyses the addition of both GlcNac and GalNac di:saccharide(s) units to a
                                                                                                                                                                                                                                                                                    AAU72923 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A novel polyglycosyltransferase (PGTase) (AAW06576) from Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 2A-C; 38pp; English.
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                                                 intection;
                                                                         Meningitis; virulence;
                                                                                                                                                                                 12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-052351/05
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                                                                                                                                                                                                                                                                                                                                                                                                                    PSGAWLDFAADGRMRRLFTLRQYFGILYRLIK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLTDLLDFLTDRVMRKLFAAPQYRKILKKMLR 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IAMGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNPIHNNTMIMRRSVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QKTARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEKDLPEEDFERARRFLYQCFKRTDTP
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213; Conser
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                                                                                                                             meningitidis virulence
                                           ; virulence; gene; antibacterial; vaccine;
Gram-negative bacteria; antimicrobial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348 AA;
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                                                                                                                                                                            (first entry)
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Pred. No. 5.3e
34; Mismatches
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5.3e-102;
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Neisseria meningitidis

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RESULT 6
AAW89332
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Best Local S
Matches 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a peptide (I) encoded by an operon (II) of Meisseria meningitidis including virulence genes, or a related molecule having a 40% sequence similarity at the peptide or nucleotide level in a Gram-negative bacterium, or its functional fragment, for therapeutic or diagnostic use. (I) and (II) are useful in the manufacture of a medicament for treating or preventing a condition (e.g., meningitis) associated with infection by Neisseria or Gram-negative bacteria. The product is useful for veterinary treatment and in a screening assay for the identification of an antimicrobial drug. The vaccines have prophylactic applications. AAU72911-AAU73014 represent N. meningitidis virulence proteins of the invention.
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                                  26-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 60-61; 423pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptide encoded by operon including virulence genes of Neisseria meningitidis, useful as vaccine component for treating or preventing
                                                                 AAW89332;
                                                                                              AAW89332 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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hes 208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MQPLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQBQDGRI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002-066593/09
DB; AAS97208.
                                                                                                                                                                                                                                                                                                                       GLRFDPAYIHAEDYKFWYEAGKLGRLAYYPEALVKYRFHQDQTSSKYNLQQRRTAWKIKE
                                                                                                                                                                                                                                                                                                                                                                                   MGAWLEVLSEENNKSVLAAIARNGAIWDKPTRHEDIVAVFPFGNPIHNNTMIMRRSVIDG 180
                                                                                                                                                                           GAWLDFAADGKMRRLFTMRQYFGILHRLIK 330
                                                                                                                                                                                                          TDLLDFLTDRVMRKLFAAPQYRKILKKMLR 330
                                                                                                                                                                                                                                         TARNDFLQSMGFKTRFDSLEYRQIKAVAYELLEKHLPEEDFERARRFLYQCFKRTDTPPA
                                                                                                                                                                                                                                                                    EIRAGYWKAAGIAVGADCLNYGLLKSTAYALYEKALSGQDIGCLRLFLYEYFLSLEKYSL 300
                                                                                                                                                                                                                                                                                                     GLRYNTERDWAEDYQFWYDVSKLGRLAYYPEALVKYRLHANQVSSKYSIRQHEIAQGIQK
                                                                                                                                                                                                                                                                                                                                                                   MGAWLEVLSEEKDGNRLARHHRHGKIWKKPTRHEDIADFFPFGNPIHNNTMIMRRSVIDG
                                                                                                                                                                                                                                                                                                                                                                                                                               KILAQAQNSGLIPSLNIGLDELAKSGMGEYIARTDADDIAAPDWIEKIVGEMEKDRSIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LQPLVSVLICAYNVEKYFAQSLATVVNQTWRNLEILIVDDGSTDGTLAIAKDFQKRDSRI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 63.0
08; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346
                                  (first entry)
                                                                                            peptide;
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Pred. No. 6e-101;
6; Mismatches 86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346;
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RESULT 7
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           A method has been developed of expressing a glycosyltransferase in a host cell. The method comprises introducing into the host cell a nucleic acid encoding the glycosyltransferase and incubating the host cell under conditions appropriate for expression of the glycosyltransferase, where the host cell substantially lacks a protease that cleaves polypeptides between two consecutive positively charged amino acid residues. The glycosyltransferase can be used in in vitro production of oligosaccharide structures which are potential therapeutic agents for use in the manipulation of cell-cell recognition events, particularly adhesion of bacteria and viruses to mammalian cells and leukocyte-endothalial cell interaction through selectins in inflammation. The method provides more readily recoverable active glycosyltransferases than prior art methods involving mammalian glycosyltransferases. The present sequence represents a C-terminal peptide from Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expressing high levels of glycosyltransferases - comprises use of either host cells deficient in proteolytic enzymes or modified glycosyltransferase genes deleted in a proteolytic recognition site
                                                                                                                                                                                                                                  AAB96313 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycosyltransferase;
                            27-OCT-2000
                                                       FR2792651-A1
                                                                                  Pyrococcus abyssi
                                                                                                               Hyperthermophilic archaeon; hyperthermophilic protein
                                                                                                                                            Putative glycosyltransferase, involved in cell wall biogenesis
                                                                                                                                                                          29-OCT-2001
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                                                                                                                                                                                                                                                                                                                                    285 RLFLYEYFLSLEKYSLTDLLDFLTDRVMRKLFAAPQYRKILKKMLRPWKY 334
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                                                                                                                                                                                                                                                                                                                                                                            14.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteolytic enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                Mismatches
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21-APR-1999;

99FR-0005034

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RESULT 8
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Best Local S
Matches 83
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Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436.
                             biosynthesis;
                                      EPS plasmid; Lactococcus lactis subspecies cremoris Ropy352; exopolysaccharide; EPS352; milk; thickener; glycosyltransferase;
                                                                                   Epsn.
                                                                                                                                                                  AAB47426 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleotide sequences isolated from proteins useful in industry -
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Querellou J,
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Lactococcus lactis
                                                                                                              17-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                VIDGGLRFDPAYIHAEDYKFWYEAGKLGRLAYYPEALVKYRFHQDQTS---SKYNLQQRR 233
                                                                                                                                                                                                                                                                                                                                                                                                             VYGGFYY-----VSQDGRILGKRLPKHRGDIYSHLLKENFIGSPTLLIRRE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                   IAMGAWLEVLSEENNKSVLAAIARNGAIWDK--PTRHEDIVAVFPFGNPIHNNTMIMRRS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPIVSVIIPTYNRANLLRRAIASVLNQKFKDFELIVVDDASTDNTPEVVESI--EDGRIR 60
                                                                                                                                                                                                                                                                                                                                                      CFKKAGLFDPRLSSSQDWDMWLRIARYYKFDYVDEIIAKYYVHGKQISFNMKKYIPGRER
                                                                                                                                                                                                                                         -----LNLENYMI
                                                                                                                                                                                                                                                                   LFLYEYFLSLEKYSL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEME---KDRSI 118
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Weissenbach
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                           fruit
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                                                                                                                                                                    Protein;
                           juice.
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26.3%; Pred. No. 6.1e-17;
tive 48; Mismatches 128
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RESULT 9
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AC AAG9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in AAB47426-27 are encoded by a fragment of the EPS CD plasmid derived from L. lactis subspecies cremoris Ropy352. The EPS CD plasmid is about 32 kb in size and encodes at least 13 active genes. CC The enzymes encoded by these genes allow the bacteria to produce an CD exopolysaccharide, designated EPS352. When EPS352 is expressed in or CD can be compared to milk, it imparts highly desirable sensory characteristics to CD compared to milk, including making the milk very thick, with a very smooth CD compared to the milk very thick, with a very smooth CD compared to the milk very thick, with a very smooth CD compared to the milk very thick of the CD compared to the CD compared to EPS352 biosynthesis. L. lactis cremoris Ropy352 is convolved in EPS352 biosynthesis. L. lactis cremoris Ropy352 is CD compared with the USDA-ARS-NCAUR-NRRL as deposit accession number CD compared to the CDA-ARS-NCAUR-NRRL as deposit accession number CD compared to the CDA-ARS-NCAUR-NRRL as deposit accession number CD compared to the CDA-ARS-NCAUR-NRRL as deposit accession number CD compared to the CDA-ARS-NCAUR-NRRL as deposit accession number CD compared to the CDA-ARS-NCAUR-NRRL as deposit accession number CDA-ARS-NCAUR-NRRL as deposi
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAH43198
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                                                                          TSSKYN 228
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    ASKKFS
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                                                                                                                                                                                                                                                                                                                      YYICKGKNIYPNVNNDLLECEGLLSRDKTMRSILSDTGFKGFVW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -NTKNLGVSHARNYGIDR----ASGSYIMFLDPDDTYDKSYCLEMIGLINKFNADVVMSN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LISITYPYYNSEKYLRAAIHSLLNQTYQNIEVILINDGSTDGSQELISSFQKKDKRIKLY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61;
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US DEPT OF AGRICUI
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                                                                                                                                                         -TRIFRKNVIN-NVKFNESINYLEDMLFNISIVHNARIIAYTNKRHYFYLQREDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Knoshaug
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2000US-0241098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.7%;
24.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 223.5; DB 2
Pred. No. 8.4e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JA,
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                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                 analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organic
                                                                                                                                                                                                                                                                                                                                                                                                                                      European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coryneform bacterium; amino acid synthesis; vitamin; saccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUN-2001
222 WIILKRRMELASFLKRSPVRQIFLNFIWYGAQVTRYLGLRKAGFMTGY
                                  235
                                                                     164
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                                                                                                                                                                    121
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                                AWKIKEEIR-AGYWKAAGIA------VGADCLNY-GLLKS---TAY
                                                                                      VID--GGLRFDPAYIHAEDYKFWYEAGKLGRLAYYPEALVKYRFHQDQTSSKYNLQQRRT
                                                                                                                                                                                                                                   RIISNPRNLGFTASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 120
                                                                                                                                                                                                                                                                                                    PLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPA--IARHFQEQDGRI 60
                                                                VVEQIGGYSLE--MTRSQDYELFLRLSKIGAIGYLDESLSSYRIHGGQHSRKTSPFKKYT
                                                                                                                                                                 MGAWLEVLSEENNKSVLAAIARNGAIW----DKPTRHEDIVAVFPFGNPIHNNTMIMRRS 176
                                                                                                                                                                                                   KIVEQKIRQGTPTSLNNGI----KASDGQLIARLDSDDLAAPSRLSKQEEFLRNHPYIIC
                                                                                                                                                                                                                                                                    PLISVVIPTIAYDEYCSQSIKSVCEQNYENWQIVLV----LDGAPIKDVPQWVKEHE-RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO: 3905; 246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                       274 AA;
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Senoh A, Ik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein fragment SEQ ID
                                                                                                                                                                                                                                                                                                                                                   12.4%; Score 219.5; DB 22; 27.1%; Pred. No. 1.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ikeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ando S, Hayas
da M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                57; Mismatches
                                                                                                                                   ·HGKIFGQSADLPT-SQDIRQILLVKNPIIHSSVMYRKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO: 3905
                                                                                                                                                                                                                                                                                                                                     108;
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                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                   Length 274;
 269
                                                                                                                                                                                                                                                                                                                                     45;
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                                                                                                                                                                                                                                                                    60
                                                                                                                                   163
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μ

MOPLVSYLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGRI 60

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RESULT 10
AAY54072
ID AAY54
                                                                   AAY54065-74 represent enzymes involved in the biosynthesis of CC exopolysaccharides (EPS). These enzymes are designated EPS1-EPS10. and CC exopolysaccharides (EPS). These enzymes are isolated CC are encoded by open reading frames eps1-eps10. The enzymes are isolated CC from Streptococcus thermophilus strain Sfi39. The proteins are used CC in a method for the synthesis of EPS, which includes at least one step CC of forming a bond (alpha or beta-isomer) between C-1 (carrying the creducing aldehyde function, of an activated D-galactose pyranose), and CC a phosphate on a lipophilic or proteinaceous primer. Stepwise synthesis CC of EPS occurs with, in each step, addition of a new sugar unit, through CC its hemi-acetyl function, to an alcoholic hydroxyl of a second sugar CC unit, present at the end of a chain of sugar residues bonded to the CC primer. EPS1 to EPS4 are used to elongate the EPS chain, and to regulate CC EPS production, EPS5 creates new bonds between saccharides, EPS6 is used in the biosynthesis of EPS, EPS7 and EPS8 are beta-glycosyltransferases, CC conversion of a pyranose form of a beta-p-galactose to the furanose
     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-APR-1998;
22-APR-1998;
22-APR-1998;
                                                                                                                  conversion of a pyranose form of a beta-D-galactose to the furanose form. The EPS enzyme are used to improve properties of foods, particularly fermented milk products such as yoghurt and cheese,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY54072 standard;
                                                                   Sequence
                                                                                                 e.g. their organoleptic properties and flavour stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 105-106; 162pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant enzymes for synthesis of exopolysaccharides, particularly in lactic acid bacteria, for improving properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAZ45258, AAY54072, AAY54073, AAY54074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-097267/08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activated D-galactose pyranose; saccharide; beta-glycosyltransferase;
transporter; food; fermented milk product; yoghurt; cheese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Exopolysaccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enzyme EPS8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        flavour stability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fermented milk products
                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPS7; EPS8; EPS9;
     81;
                    Similarity
                                                                     316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Germond JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98EP-0201310.
98EP-0201311.
98EP-0201312.
                                                                     AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organoleptic property
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                 12.2%; 23.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         involved in exopolysaccharide biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPS10; Streptococcus the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lamothe
   59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316
 Score 215; DB 21;
Pred. No. 6.2e-14;
9; Mismatches 105
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     105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPS3;
   Indels 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPS4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of.
Gaps
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AAY43767-76 represent the proteins encoded by the eps operon of Streptococcus thermophilus Sfi39. The operon contains 10 open reading frames, and encodes enzymes (eps1, eps2, eps3, eps5, eps6, eps7, eps8, eps9 and eps10) that are involved in the biosynthesis of exopolysaccharides (EPS). The enzymes catalyse the formation of specific intersugar bonds. The enzymes catalyse a process that includes at least one step of forming a bond (in alpha or beta anomeric form) between C1, carrying the reducing aldehyde group of an activated D-Galp (galactose in pyranose form), and a phosphate group on a lipophilic or proteinaceous primer. The enzymes are used to produce EPS that have antitumor or probiotic properties or are used in foodstuffs to improve
                                                                                                                                                                             Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eps3; eps4; eps5; eps6; eps7; eps8; eps9; eps10;
exopolysaccharide biosynthesis; EPS; intersugar
                                                                                                                                                                                                                     New recombinant enzymes for biosynthesis of exopolysaccharides having e.g. antitumor or probiotic properties or useful in fermented milk
                                                                                                                                                                                                                                                                                                           Stingele F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY43774 standard;
                                                                                                                                                                                                                                                                                                                                                                  22-APR-1998;
22-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09954475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of eps8 of Streptococcus thermophilus Sfi39
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                                                                                                                                                                                                                                                                                                                                                                                                22-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                            22-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  operon; Streptococcus thermophilus Sfi39;
                                                                                                                                                                                                                                                               2000-013255/01.
DB; AAZ30355, AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTKTTKNAQK - :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VWSSIYRLDFINSNHIRFTPGILF-EDADFTIRAYMLAKLVATSPEPNYAYRINRPGSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGAWLEVLSEENNKSVLAAIARNGAI ••••-WDKPTRHEDIVAVFPFGNPIHNN••••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVI-NQKNQGLSVARNTGID----AATGKYIAFVDADDKIKPDFVSSLYQIADKTGADIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCLRLFLYEYFLSLEKYSLTDLLDFLTDRVMRKLFAAPQYRKILKKMLRPW 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTSSKYNLQQRRTAWKIKEEIRAGYWKAAGIAVGADCLNYGLLKSTAYALYEKALSGQDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---TMIMRRSVIDGG-LRFDPAYIHAEDYKFWYEAGKLGRL-AYYPEALVKYRFHQD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGSFRDF-----LDQFLSSNISFV
                                                                                                                                                                                                                                                                                                                                       SOC
                                                                                                                                                                             Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----FISMLKHEKSDVLCSL---ILKSIYAC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          foodstuff;
                                                                                                                                                                                                                                                                                                                                       PROD
                                                                                                                                                                                                                                                                                                           Germond JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                             106-107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thermophilus.
                                                                                                                                                                                                                                                                                                                                                                  98EP-0201311.
98EP-0201312.
                                                                                                                                                                                                                                                                                                                                                                                                98EP-0201310
                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-EP03011.
                                                                                                                                                                                                                                                                                                                                       NESTLE
                                                                                                                                                                                                                                                              AAY43774, AAY43775, AAY43776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organoleptic quality; flavour; acidified milk product.
                                                                                                                                                                           163pp; French
                                                                                                                                                                                                                                                                                                                                       SA
                                                                                                                                                                                                                                                                                                           Lamothe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                           <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --MSLSEEKIISQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -MRDW 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eps1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156
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RESULT 12
AAY96213
ID AAY96
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PA XXX PA DR XXX PA DR XXX PA PA XXX PA PA XXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QΥ
                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                 WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organoleptic qualities and flavour. When expressed by lactic acid bacteria, EPS impart a free-flowing character and/or a smooth, cretexture to acidified milk products (yoghurt or cheese).
                       Claim 15;
                                                                                                                                                                                      11-NOV-1998;
01-APR-1999;
                                                                                                                                                                                                                                                                                                                                        Chondroitan synthase; CS;
                                                                                                                                                                                                                                                                                                                                                                  P. multocida chondroitan synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY96213 standard;
                                                            acceptor,
                                                                                                                                    DeAngelis
                                                                                                                                                                                                                           10-NOV-1999;
                                                                                                                                                                                                                                                    18-MAY-2000
                                                                                                                                                                                                                                                                            WO200027437-A2
                                                                                                                                                                                                                                                                                                   Pasteurella multocida
                                                                                                                                                                                                                                                                                                                              tissue
                                                                                                                                                                                                                                                                                                                                                                                           17-AUG-2000
                                                                                                                                                           (OKLA ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _
                                          l method for the enzymatic transfer of sugar molecules
ptor, useful for synthesis of e.g. polysaccharide bioac
delivery systems, including hybrid molecules -
                                                                                               2000-376319/32.
DB; AAA27449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGAWLEVLSEENNKSVLAAIARNGAI------WDKPTRHEDIVAVFPFGNPIHNN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MQPLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGRI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MNPLISIIVPTYNVEKYIRTCIESILAQTYRNIEVIIVNDGSTDQSLAVISDLICSHHNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCLRLFLYEYFLSLEKYSLTDLLDFLTDRVMRKLFAAPQYRKILKKMLRPW 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTKTTKNAQK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QTSSKYNLQQRRTAWKIKEEIRAGYWKAAGIAVGADCLNYGLLKSTAYALYEKALSGQDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VWSSIYRLDFINSNHIRFTPGILF-EDADFTIRAYMLAKLVATSPEPNYAYRINRPGSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --TMIMRRSVIDGG-LRFDPAYIHAEDYKFWYEAGKLGRL-AYYPEALVKYRFHQD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGSFRDF - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVI-NQKNQGLSVARNTGID----AATGKYIAFVDADDKIKPDFVSSLYQIADKTGADIV
                                                                                                                                                                                                                                                                                                                              abrasion;
                                                                                                                                    PL;
                      Page 85; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     316 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                             OKLAHOMA STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -FISMLKHEKSDVLCSL---ILKSIYAC--
                                                                                                                                                                                      98US-0107929
99US-0283402
                                                                                                                                                                                                                           99WO-US26501
                                                                                                                                                                                                                                                                                                                              viscoelastic
                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.2%;
23.1%;
                                                                                                                                                                                                                                                                                                                                         enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -NGNIPKGWVPDFNVPTNYGTIV----LDQFLSSNISFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                             965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 215; DB 21; Pred. No. 6.2e-14;
                                                                                                                                                                                                                                                                                                                              replacement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             ΑĀ
                                                                                                                                                                                                                                                                                                                              hyaluronic acid; ulcer; lacement; bioadhesive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105; Indels 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -MSLSEEKIISQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a smooth, creamy
                                                           cules to an bioadhesives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221
                                                            or
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The present sequence is

the Pasteurella multocida chondroitan synthase

acid

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RESULT 13
AAM47335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PmCS. PmCS catalyses glycosaminoglycan polymerisation to produce chondroitan: a linear polysaccharide which has viscoelastic properties which makes it useful for a number of applications. Chondroitan can be used with hyaluronic acid (HA) to coat medical devices e.g. catheters ar sensors to reduce tissue abrasion. In addition, they can be used as bioadhesives for haemostatic sealing and healing of wounds and surgical incisions; and as biomaterials that provide sustained delivery of encapsulated drugs, to wounds, ulcers, injuries or surgical sites.
useful as hyaluronan
                         New chondroitin synthase gene obtained from Pasteurella multocida,
                                                      WPI; 2002-049237/06.
N-PSDB; ABA05097.
                                                                                                                                                                                                                                                                                                                              Chondroitin synthase; dermatan sulphate; eye application; joint application; mois:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM47335 standard;
                                                                                                                                                                                                                          01-NOV-2001
                                                                                                                                                                                                                                                      WO200180810-A2
                                                                                                                                                                                                                                                                                    Pasteurella multocida.
                                                                                                                                                                                                                                                                                                                                                                            Pasteurella multocida chondroitin synthase #1.
                                                                                                                                                                                                                                                                                                                                                                                                          22-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM47335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                  De Angelis PL;
                                                                                                                                (DANG/) DE ANGELIS P
                                                                                                                                                              25-APR-2000; 2000US-199538P
                                                                                                                                                                                          25-APR-2001; 2001WO-US13395
                                                                                                                                                                                                                                                                                                                   wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIRAGYWKAAGIAVGADCLNYGLLKSTAYALYEKALSGQDIGCLRLFLYEYFLSLE---K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAMG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGRIRI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YIFNKTAEYQEEMDMLK 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YSLIDLLDFLIDRVMRK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---FNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLREDPAYIHAEDYKFWYEAGKLGRLAYYPEALVKYRFHQDQTSSKYNLQQRRTAWKIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----VYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMI----AHHFRMFTIRAWHLTDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AWLEVLSEENNKSVLAAIARNGAIWDKPTRHEDIVAVFPFGNPIHNNTMIMRRS--VIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSKPN--GGIASASNAAVSFAK---GYYIGQLDSDDYLEPDAVELCLKEFLKDKTLAC--
                                                                                                                                                                                                                                                                                                                dressing; biocompatible film.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------KLGIQKKNHFVVVNQSLNRQGI---NYYNYDKFDDLDESRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                              joint application; moisturiser;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.8%;
23.7%;
                                                                                                                                ۲
         polysaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      965
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Pred. No. 1.5e-12;
3; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ÃĀ.
          substitute
                                                                                                                                                                                                                                                                                                                              chondroitin sulphate polymer;
turiser; drug delivery;
          'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 965;
          medial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
          or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60;
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            cosmetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT 14
AAY06212
ID AAY06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          applications, for example in eye or joint applications, for moisturise; or wound dressings. The enzyme may be used in covalently coupling specific drugs, proteins or toxins to the structurally modified chondroitin for general or targeted drug delivery or radiological procedures, covalently cross linking the hyaluronic acid itself or to other supports to achieve a gel or other three dimensional biomaterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with stronger physical properties, and covalently linking hyaluronic to a surface to create a biocompatible film or monolayer. The present sequence is one version of the protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to the coding sequence of the Pasteurella multocida chondroitin synthase. A chondroitin polysaccharide may be used as a hyaluronan polysaccharide substitute in medial or cosmetic
                              26-OCT-1998;
31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                           Hyaluronate synthase; pmHAS;
                                                                                                                                                                                                                      Pasteurella multocida hyaluronate synthase pmHAS
                                                                                                                                                                                                                                                     16-AUG-1999
                                                                                                                                                                                                                                                                                  AAY06212;
                                                                                                                                                                                                                                                                                                               AAY06212 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     applications, e.g.
(OKLA ) UNIV
                                                                         30-OCT-1998;
                                                                                                   14-MAY-1999
                                                                                                                                  WO9923227-A2
                                                                                                                                                               Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         wound dressings
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AWLEVLSEENNKSYLAAIARNGAIWDKPTRHEDIVAVFPFGNPIHNNTMIMRRS--VIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLYSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGRIRI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---FNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLREDPAYIHAEDYKFWYEAGKLGRLAYYPEALVKYRFHQDQTSSKYNLQQRRTAWKIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----VYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMI----AHHFRMFTIRAWHLTDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSKPN--GGIASASNAAVSFAK---GYYIGQLDSDDYLEPDAVELCLKEFLKDKTLAC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAMG 122
                                                                                                                                                                                                                                                                                                                                                                                       YIFNKTAEYQEEMDMLK
                                                                                                                                                                                                                                                                                                                                                                                                                     YSLTDLLDFLTDRVMRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EIRAGYWKAAGIAVGADCLNYGLLKSTAYALYEKALSGQDIGCLRLFLYEYFLSLE---K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      965 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
OKLAHOMA STATE
                                                                                                                                                                                                                                                     (first entry)
                             98US-0178851
97US-0064435
                                                                         98WO-US23153
                                                                                                                                                                                                                                                                                                               Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.8%;
23.7%;
                                                                                                                                                                                                                                                                                                                                                                                       694
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                                                                                                                                                                                                                                                                                                               972
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                                                                                                                                                                                           hyaluronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                           acid; hyaluronan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tor moisturiser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60;
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                                                                                                         RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dependence, and different Km values compared with the HAS enzymes of Streptococcus equisimilis (see AAY06206) and Streptococcus pyogenes. Km values are about 2- to 3-fold lower for UDP sugars, and Vmax values are about 2- to 3-fold higher. The invention
               01-FEB-2000
                                              AAY43099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               provides recombinant vectors containing hyaluronate synthase DNA, especially S. equisimilis hyaluronate synthase DNA (see AAX58841) and prokaryotic or eukaryotic host cells which produce the enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             different kinetic optima with respect to pH and metal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 123-125; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding hyaluronate synthase for production of hyaluronic acid with controlled molecular weight and targeting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
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                                                                          AAY43099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is present sequence represents the hyaluronate synthase Pasteurella multocida Carter Type A. The pmHAS enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 PLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGRIRI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   its hyaluronic acid product, particularly a product with fied structure or molecular size. The hyaluronic acid produced
                                                                                                                                                                                                                                                                                                                                                                                                  ---FNEKIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVN
                                                                                                                                                                                                                                                                                                                                                                                                                              GLRFDPAYIHAEDYKFWYEAGKLGRLAYYPEALVKYRFHQDQTSSK--------
                                                                                                                                                    LTHDWIEKINAHPPFKKLIK
                                                                                                                                                                                                                TSNRLIKTEAHLSNINKLSQLNLNCEYIIFDNHDSLFVKNDSYAY --
                                                                                                                                                                                                                                                                                                                                    QSLNRQGITYYNYDEFDDLDESRKYIFNKTAEYQEEIDILKDIKIIQNKDAKIAVSIFYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----VYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMI----AHHFRMFTIRAWHLTDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AWLEVLSEENNKSVLAATARNGATWDKPTRHEDIVAVFPFGNPIHNNTMIMRRS--VIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSKPN--GGIASASNAAVSFAK---GYYIGQLDSDDYLEPDAVELCLKEFLKDKTLAC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAMG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 499
                                                                                                                                                                               LTDRVMRKLFAAPQYRKILK 326
                                                                                                                                                                                                                                           ---GLLKSTAYALYEKALSGQDIGCL-----RLFL----YEYFLSLEKYSLTDLLDF
                                                                                                                                                                                                                                                                         NTLNGLVKKLNNIIEYNKNIFVIVLHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYY
                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is purer than that produced by conventional methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           972 AA;
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              (first entry)
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21.8%;
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                                                                            972
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                                                                                                                                                                                                                                                                                                        --KIKEEIRAGYWK-AAGIAVGADCLNY
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stabilisation of recombinant proteins and in cosmetics. The HS nucle acids can also be used to develop agents to block capsule synthesis pathogens and act as antibiotics. The avirulent P. multocida strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        containing the PmHAS nucleotide sequence which can be used to express PmHAS in a foreign host. The HS nucleic acids can be used for the production of HA. Also, specific changes to the HS coding sequence can result in the production of HA having a modified size distribution or structural configuration and functional properties. The HA products can be used in e.g. drug delivery, angiogenesis and wound healing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence. Hyaluronic acid (HA) or hyaluronan, is a polysaccharide that serves both structural and recognition roles in higher animals. Bacter produce extracellular capsules of HA which mimic their host HA and aid escape from a host immune response. The invention includes a vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drug delivery;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P. multocida hyaluronate synthase (PmHAS) amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 70; Fig 20; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and for diagnostic applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated hyaluronate synthase nucleic acids, used for production of hyaluronic acid, for developing antibiotics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ35589.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-013032/01.
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26-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be used as
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   661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 PLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGRIRI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is the Pasturella multocida hyaluronate synthase (PmHAS) amino
QSLNRQGITYYNYDEFDDLDESRKYIFNKTAEYQEEIDILKDIKIIQNKDAKIAVSIFYP
                                                                                                                                                                                      GLRFDPAYIHAEDYKFWYEAGKLGRLAYYPEALVKYRFHQDQTSSK----
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                                                                                                                                                                                                                                                                                                                                                                     MSKPN--GGIASASNAAVSFAK---GYYIGQLDSDDYLEPDAVELCLKEFLKDKTLAC--
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                                                                                                                      -FNEKIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVN
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                                                            - VNLQQ
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angiogenesis; wound healing; capsule synthe
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98US-0178851.
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                                                               -RRTAW----
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re greater than or equal to the score of the result being printed,
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US-08-683-458-5
US-08-878-360-5
US-09-333-412-5
US-08-683-426-12
US-08-683-426-12
US-08-683-426-12
US-08-683-426-12
US-08-312-387B-3
US-08-312-387B-3
US-08-683-426-3
US-08-683-426-3
US-08-683-426-11
US-08-333-412-11
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Query Match Best Local S Matches 337

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Local Similarity es 337; Conserv

100.0%; Score 1764; DB 1; ilarity 100.0%; Pred. No. 1.2e-178; Conservative 0; Mismatches 0;

Indels Length

Gaps

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337; 0;

RESULT 1 US-08-312-387B-5 Sequence 5, Application US/08312387B Sequence 5, Application US/08312387B Sequence 5, Application US/08312387B Patent No. 5545553 GENERAL INFORMATION: APPLICANT: Gotschlich, Emil C. TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS INUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSEE: Klauber & Jackson STREET: 411 Hackensack Avenue CITY: Hackensack Avenue COUNTRY: USA ZIP: 07601 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DGS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/312,387B. FILING SYSTEM: DATA: APPLICATION NUMBER: US/08/312,387B. FILING DATE: July 7, 1994 CLASSIFICATION UNBER: 600-1-095 TELECHONGUNICATION INFORMATION: NAME: Jackson Esq., David A. REGISTRATION UNBER: 600-1-095 TELECHONGUNICATION INFORMATION: TELEPHONE: 201 487-5800 TELEPHONE: 201 487-5800 TELEPHONE: 201 343-1684 TELEPHONE: 201 34	ALIGNMENTS	28 201.5 11.4 702 4 US-09-437-277-1 29 199 11.3 324 1 US-08-597-236-10 30 199 11.3 324 1 US-08-597-236-10 31 185.5 10.5 281 4 US-08-961-083-200 32 162 9.2 674 4 US-08-961-083-200 33 152.5 8.6 93 4 US-08-961-083-202 34 152 8.6 93 4 US-08-961-083-202 35 150 8.5 270 4 US-08-961-083-198 36 138 7.8 358 4 US-09-134-001C-5633 37 131.5 7.5 727 4 US-09-134-001C-4067 38 116.5 6.6 727 4 US-09-134-001C-4067 39 116.5 6.6 418 4 US-09-134-001C-4051 40 99.5 5.6 1410 3 US-09-355-409-3 41 99.5 5.6 1410 4 US-09-568-480-3 45 99.5 5.6 1410 4 US-09-568-480-3 45 99.5 5.6 1410 4 US-09-568-480-3 45 99.5 5.6 1410 4 US-09-568-480-3
DING THEM		Sequence 1, Appli Sequence 10, Appl Sequence 106, Appl Sequence 200, App Sequence 201, Appl Sequence 521, Appl Sequence 521, Appl Sequence 5633, Appli Sequence 168, App Sequence 4067, App Sequence 4067, App Sequence 3, Appli Sequence 3, Appli

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                                                                                                  Query Match
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                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                        NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/312,387
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TELEX: 133521
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CITY: Hackensack
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MQPLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGRI 60
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                                                              Score 1764; DB 1;
Pred. No. 1.2e-178;
Mismatches 0;
                                                                                                  Length
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Patent No. 5798233
GENERAL INFORMATION:
                                                                        Query Match
Best Local Similarity
                                                            Matches
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acid
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
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APPLICATION NUMBER:
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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CITY: H
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CLASSIFICATION: 435
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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EIRAGYWKAAGIAVGADCLNYGLLKSTAYALYEKALSGQDIGCLRLFLYEYFLSLEKYSL
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                                                                        Score 1764; DB 1; Pred. No. 1.2e-178;
                                                         Mismatches
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                                                                                      Length
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                                                                                                                            TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid
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     Query Match
Best Local Similarity
Matches 337; Conserv
                                                                                                                                                                                                                                       NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/878,360
FILING DATE: 18-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Klauber & Jackson
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Bolon
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STATE: New Jersey
                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
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100.0%; Score 1764; DB 2; ilarity 100.0%; Pred. No. 1.2e-178; Conservative 0; Mismatches 0:
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                                        Length 337;
     Indels
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     Gaps
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                                                                      ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ US-09-333-412-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09333412 Patent No. 6342382 GENERAL INFORMATION:
Query Match
Best Local Similarity
Matches 337; Conserv
                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Jun-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/312,387 FILING DATE: July 7, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid
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ADDRESSEE: Klauber & Jackson
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TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
OLIGOSACCHARIDES, AND GENES ENCODING THEN
                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                             NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1-095
100.0%; ilarity 100.0%; Conservative C
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Score 1764; DB 4;
Pred. No. 1.2e-178;
Mismatches 0;
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                                                                                                             Matches
                                                                                                                                                                             Query Match
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APPLICANT: Gotsch
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,387B
FILING DATE: JULY 7, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
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                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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TELEPHONE: Z
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                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                             Local
1 MQPLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGRI 60
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                                                                                                                                          h 99.8%;
Similarity 99.7%;
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VENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                          Conservative
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                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    600-1-095
                                                                                                   Score 1761; DB 1;
Pred. No. 2.4e-178;
1; Mismatches 0;
                                                                                                                                                                      Length 337;
                                                                                                          Indels
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US-08-683-426-12
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APPLICANT: Gotschlich, Emil C.
   Matches
                                Query Match
                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: GLYCUSIA......
TITLE OF INVENTION: OLIGOSACCHARIDES,
                                                                                                                                                                                                         NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                              TELEFAX: ZVZ
TELEFAX: ZVZ
TEX: 133521
SE/
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                                                                                                        TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
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 Local Similarity
mes 336; Conserv
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Score 1761; DB 1;
Pred. No. 2.4e-178;
1; Mismatches 0;
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                                Length 337;
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RESULT 8
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                                                     ; TOPOLOGY: 1; MOLECULE TYPE: US-08-683-458-12
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Best Local
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    Matches
                                                                                                                                 TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                         NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Jackson Esq., Davi
                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: Septemb
CLASSIFICATION: 435
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APPLICATION NUMBER: US/08/683,458
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 435
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STATE: New Jersey
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    336;
               Similarity
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                                                                                              amino acid
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  Conservative
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                                                                                                                                                                                                                                                                       September 26, 1994
              99.8%;
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            Score 1761; DB 1;
Pred. No. 2.4e-178;
  Mismatches
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                         Length 337;
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APPLICANT: Gotsch
                       MOLECULE TYPE:
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                                        TOPOLOGY:
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                                                 amino acid
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Sequence 12, Application US/08878360 Patent No. 5945322
                                                                                                         TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 600-1-095B TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING:
                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/878,360
FILING DATE: 18-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/683,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
FILING DATE: Septemb
CLASSIFICATION: 435
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STATE: New Jersey
                                                                                                                                                                                                                                          NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
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protein
                                                                                                                                                                                                                                                                                                                                     September 26, 1994
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                                                                                                                                                                                                                                                                                                                                                               08/312,387
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Score 1761;

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Length 337;

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US-08-478-140B-5
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GENERAL INFORMATION:
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                                                                                                         TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                 MOLECULE TYPE:
                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                             REFERENCE/DOCKET NUMBER: 71
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 30,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: JOHNSON, KARL F. APPLICANT: ROTH, STEPHEN
                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1155 Ave
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
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                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/478,140B FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                   TOPOLOGY:
                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                    LENGTH:
                                                                                                                                               TELEFAX:
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                                                                       337 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BUCZALA, STEPHANIE L.

NVENTION: METHOD OF TRANSFERRING AT LEAST TWO
NVENTION: SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSFERASE,
NVENTION: POLYGLYCOSYLTRANSFERASE AND GENE ENCODING A
NVENTION: POLYGLYCOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1155 Avenue of the Americas
                                                                                                                                               (212) 869-9741/8864
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1; Mismatches 0;
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US-09-333-412-12
US-09-333-412-12
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Patent No. 6342382
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best
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                                                                                     INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
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NAME: Jackson Esg., David A.
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
TELEGMUNICATION INFORMATION:
TELEFRAN: 201 487-8800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Jun-1999
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                  TOPOLOGY: linear MOLECULE TYPE: protei
                 MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/312,387 FILING DATE: July 7, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 411 Hackensack Avenue
                                                                                                                                              TELEX: 133521
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                  ID NO:
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US-09-338-943-5
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Patent No. 6379933
GENERAL INFORMATION:
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Best Local Similarity
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                                     TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COCCURRATING SYSTEM: PC-DOS/MS-DOS
   SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acid
                                                                                                           REFERENCE/DOCKET NUMBER: 71 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                   FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                         TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                 NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RIISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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VENTION: METHOD OF TRANSFERRING AT LEAST TWO
VENTION: SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSFERASE,
VENTION: POLYGLYCOSYLTRANSFERASE AND GENE ENCODING A
VENTION: POLYGLYCOSYLTRANSFERASE

POLYGLYCOSYLTRANSFERASE
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 amino acids
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99.7%;
                                                                                                                                          30,742
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of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1761; DB 4;
Pred. No. 2.4e-178;
                                                                                                                              7188-017
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-338-943-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-08-312-387B-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08312387B Patent No. 5545553
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                                                                                       TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Gotsch
                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                            TELECOMMUNICATION INFORMATION TELEPHONE: 201 487-5800
                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., Davi
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LITY: Hackensack
STATE: New T
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                                                                                                         TELEPHONE: ZU1 ...
TELEPHONE: ZU1 ...
201 343-1684
                                                                                                                                                                              NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08 FILING DATE: July 7, 1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U
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                  TOPOLOGY:
                                TYPE: amino acid
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                                                    LENGTH:
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                                                    348 amino acids
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VENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
VENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
'EQUENCES: 12
                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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Pred. No. 2.4e-178;
1; Mismatches 0;
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                                                             TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
                 SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
                                                                                                  TELEFONMUNICATION INFORMATION:
TELEFHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
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TITLE OF INVENTION: GLYCOSYLTRANSFERAS
TITLE OF INVENTION: OLIGOSACCHARIDES,
                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRAFION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
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STATE: New Jersey
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    amino acid
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GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
                                                                                                                                                                                                                                                                                                 08/312,387
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US-08-683-458-3
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Best Local Similarity
Matches 214; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                 TELEX: 133521
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                     APPLICATION NUMBER: 08/3
FILING DATE: September 2
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., Davi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THE
                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: UFILING DATE: CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                 TELEPHONE: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
                                                                                                                                              NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1-095A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 KILAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSI 120
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  LENGTH:
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348 amino acids
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Pred. No. 7.3e-103;
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Search completed: December 2, 2002, 12:03:15 Job time : 13.544 secs
                                                                                                                                                                                                                                                                                                                                    Query Match 59.5%; Score 1049; DB 1; Length 348; Best Local Similarity 64.5%; Pred. No. 7.3e-103; Matches 214; Conservative 33; Mismatches 83; Indels 2; Gaps
                                                                                                                                                                                          299 SLTDLLDFLTDRVMRKLFAAPQYRKILKKMLR 330
                                                                                                           239 KEEIRAGYWKAAGIAVGADCLNYGLLKSTAYALYEKALSQQDIGCLRLFLYEYFLSLEKY 298
                                               301 PSGAWLDFAADGRMRRLFTLRQYFGILYRLIK 332
                                                                                              241 QKTARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEKDLPEEDFERARRFLYQCFKRTDTP 300
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Minimum DB
Maximum DB
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Perfect score:
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                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/U
2: /cgn2_6/ptodata/1/pubpaa/U
3: /cgn2_6/ptodata/1/pubpaa/U
4: /cgn2_6/ptodata/1/pubpaa/U
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: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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            12 US-10-007-267-5
12 US-10-007-267-12
13 US-10-007-267-13
14 US-10-007-267-13
15 US-09-924-358-29
16 US-09-9767-041-36
17 US-09-767-041-36
17 US-09-767-041-36
17 US-09-767-041-34
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Sequence 10, Appl
Sequence 36, Appl
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Sequence 31, Appl
Sequence 37, Appl
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Sequence 39, Appl
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US-10-007-267-5
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e 74,	185,	27, App	364	2,	2,	Sequence 275, App	Sequence 181, App	25,	12474,	Sequence 5714, Ap	33,	Sequence 41, Appl	168	8	Sequence 883, App	sequence 34, Appr	٥	4.	e 7,	7.4.7	e 19 e 7, e 4,	e 10 e 19 e 4, e 4,	e 4950 e 1051 e 198, e 198, e 7, Ap e 4, Ap	e 20 e 10 e 19 e 7, e 4,	e 10 e 17 e 17 e 17

ALIGNMENTS

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Sequence 5, Application US/10007267
Patent No. US20020127682A1
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
APPLICANT: Gotschlich, Emil C.
OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
ULIGOSACCHARIDES, AND GENES ENCODING THEM
                                                   INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Jun-1999
APPLICATION NUMBER: 08/312,387
FILING DATE: July 7, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/007,267 FILING DATE: 03-Dec-2001 CLASSIFICATION: <Unknown>
                                                                                                       TELEX: 133521
                                                                                                                                                                                                            NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1-095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New Jersey COUNTRY: USA
TYPE: amino acids
                                                                                                                                TELEFAX: 201 343-1684
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Patent No. US20020127682A1
GENERAL INFORMATION:
APPLICANT: GOTSChlich, Emil C
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TELEX: 13:
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Local Similarity 100.0%;
les 337; Conservative (
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                                                    RAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Jun-1999
APPLICATION NUMBER: 08/312,387
FILING DATE: July 7, 1994
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
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                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/10/007,267
FILING DATE: 03-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OPERATE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Hackensack
STATE: New Jersey
                                   TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                      07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gotschlich, Emil C.
NVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
OLIGOSACCHARIDES, AND GENES ENCODING THEM
 133521
SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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Pred. No. 1.7e-166;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                              Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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RESULT 3
US-10-007-267-3
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Best Local S
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            PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/33,412

FILING DATE: 15-Jun-1999

APPLICATION NUMBER: 08/312,387

FILING DATE: JULY 7, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-095

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/10/007,267
FILING DATE: 03-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: GLYCOSYLTRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gotschlich, Emil C.
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                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                        STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                      ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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201
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99.7%;
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Pred. No. 3.4e-166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/10007267
Patent No. US20020127682A1
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C
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Best Local
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Jun-1999
APPLICATION NUMBER: 08/312,387
FILING DATE: July 7, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gotschlich, Emil C.
APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
OLIGOSACCHARIDES, AND GENES ENCODING THEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214;
                                                                                                                                                            APPLICATION NUMBER: US/10/007,267 FILING DATE: 03-Dec-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 348 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                         STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Hackensack
REGISTRATION NUMBER: 26,742
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                   Jackson Esq., David A
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Pred. No. 6.8e-96;
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-007-267-11
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                                                                          ; OTHER INFORMATION: Consensus amino acid US-09-924-358-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-924-358-29
                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/229,300
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 29
LENGTH: 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 29, Application US/09924358 Patent No. US20020107376A1
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                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                           APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
APPLICANT: Meyers, Rachel
APPLICANT: MacBeth, Kyle
TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226, AND
TITLE OF INVENTION: 58764,
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE FAMILY MEMBERS
FILE REFERENCE: 38155-20034, 00
CURRENT APPLICATION NUMBER: US/09/924,358
CURRENT FILING DATE: 2001-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                              FEATURE:
                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
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INFORMATION FOR SEQ ID NO: 11:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KILAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSI 120
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 Conservative
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64.2%;
                 12.4%; Score 218; DB 10; 40.0%; Pred. No. 2.2e-14;
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CURRENT APPLICATION NUMBER: US/09/879,959
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 09/469,200
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 09/178,851
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
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LENGTH: 972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Weigel, Paul H
APPLICANT: Kumari, Kshama
APPLICANT: DeAngelis, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: STREPTOCOCCUS EQUISIMILIS HYALURONAN SYNTHASE GENE AND EXPRESSION TITLE OF INVENTION: IN BACILLUS SUBTILIS
                                                                                                                                                                                                                                                                                                                                                                   604
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    LTHDWIEKINAHPPFKKLIK 857
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                                                LTDRVMRKLFAAPQYRKILK 326
                                                                                          TSNRLIKTEAHLSNINKLSQLNLNCEYIIFDNHDSLFVKNDSYAY---MKKYDVGMNFSA 837
                                                                                                                                     ---GLLKSTAYALYEKALSGQDIGCL----
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                                                                                                                                     ---RLFL----YEYFLSLEKYSLTDLLDF 306
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US-09-767-041-22
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SEQ ID NO 22
LENGTH: 332
TYPE: PRT
                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                      Sequence 36, Application US/09767041
Patent No. US20020055168A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 82; Conserv
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TITLE OF INVENTION: STREPTOCOCCUS SUIS VACCINES AND DIAGNOSTIC TESTS FILE REFERENCE: 2183-4/26 CURRENT APPLICATION NUMBER: US/09/767,041 CURRENT FILING DATE: 2001-01-22 PRIOR APPLICATION NUMBER: PCT/NL99/00460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: PCT/ML99/0046(
PRIOR FILING DATE: 199-07-19
PRIOR APPLICATION NUMBER: EP98202465.5
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1998-07-22
                                                                                                                 APPLICANT:
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PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 53
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                                                                                                            Smith, Hilda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hilda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.8%; Score 208; DB 10; 22.7%; Pred. No. 6.7e-13; tive 74; Mismatches 114;
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Length 332;

92;

Gaps

18;

118 124

172

211

311

265

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APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
ITITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
ITITLE OF INVENTION: Oxford Ganglioside Mimics
ITITLE OF INVENTION: UNGARGE: US/09/816,028A
CURRENT FILLING DATE: 2001-03-21
PRIOR FILLING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: US 09/495,406
PRIOR APPLICATION NUMBER: US 09/495,406
PRIOR FILLING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 31
LENGTH: 297
TYPE: DOT
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NAME/KEY: misc_feature
OTHER INFORMATION: CPSI
US-09-767-041-36
                                                                                                                                           ; OTHER INFORMATION: beta-1,3 galactosyl transferase from C. jejuni US-09-816-028A-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-816-028A-31
                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 36
                                              Matches
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998
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TYPE: PRT
ORGANISM: Streptococcus
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                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Campylobacter jejuni
                                                                                                                                                                                       FEATURE:
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Local Similarity 25.2%;
5 VSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGRIRIIS 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KELF-----EDFRFEKGKIHEDEYFTYRLLYELEKVAIVKECLYYYVDRENSITTSSM 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTMIMRRSVIDGGLRFDPAYIHAED---YKFWYEAGKLG----RLAYYPE-----AL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRVDASGHFLTAEPLPTNQAVLSGRNVCKKLLEADG:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K-ENGGLSDARNYGISR-AK---GDYLAFIDSDDFIHSEFIQRLHEAIERENALVAVAGY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPRNIGFIASINIGIDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAMGAW 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn version 3.0
                                                Conservative
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                                                                 11.0%; 21.8%;
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                                           56;
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                                         Score 194; DB 10;
Pred. No. 1.4e-11;
6; Mismatches 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -HRFVVAC----NKLYK 169
                                                                                       Length 297
                                              Indels 126;
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; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: CPS:
US-09-767-041-35
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US-09-767-041-35
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SOFTWARE: PatentIn v
SEQ ID NO 35
LENGTH: 322
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                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                         Query Match 10.7%;
Best Local Similarity 23.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILLIAG DATE: EP98
PRIOR APPLICATION NUMBER: EP98
PRIOR APPLICATION NUMBER: EP98
PRIOR APPLICATION NUMBER: EP98
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CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: PCT/NL99/0046
PRIOR FILING DATE: 1999-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Smith, FITTLE OF INVENTION: FILE REFERENCE: 21
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135
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                                                                      IIAMGAWLEVLSEENNKSVLAAIARNGAIWDKPTRHEDIVAVFPFGNPIHNNTMIMRRSV 177
                                                                                                                                                                                  ISVIVPVYNVDKYLSSCIESIINQNYKNIEILLIDDGSVDDSAKICKEY-EKDKRVKIFF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QYRKILKKMLR 330
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ID-GGLRFDPAYIHAEDYKFWYEAGKLGRLAYYPEALVKYRFHQDQTSSK---YNLQQRR 233
                                                                                                                                              ----ISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---LLKKMQY-----NYNFNLTLLKLIEYFLLIEKYSLSSKRNVLCFKI--NIF---
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                                                                                                          TNHSGVSNARNHGI -----
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                                                                                                                                                                                                                                                                         Score 188; DB 1
Pred. No. 6e-11;
                                                                                                            -KRSTAEYIMFVDSDDVVDSRLVEKLYFNIIKSRS 110
                                                                                                                                                                                                                                                        Mismatches 132;
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                                     ----FEVNNP--NIDFEAINTV 142
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SEQ ID NO 34
LENGTH: 322
                                                                              Sequence 27, Application US/09816028A Patent No. US20020042369A1 GENERAL INFORMATION: APPLICANT: Gilbert, Michel APPLICANT: Gilbert, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 34, Application US/09767041 Patent No. US20020055168A1
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APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for
TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: PCT/NL99/0046
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SOFTWARE: PatentIn version 3.0
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NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                         YYNYVIRNSSLINQKFSINNIDLVTRLENYPFKLKREF-SHYFDAKVIKEKVKCLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGAWLEV---LSEENNKSVLAAIARNGAIWDKPTRH-----EDIVAVFPFGNPIHNN 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIDRVSYLTEHLYFYRRGILSTVNSFKEGVFLQLENLQKQVIVLF-KQIYGEDFDVSIVK 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAWKIKEEIRAGYWKAAGIAVGADCLNYGL-----LKSTAYALYEKALSGQDI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                             ----EIDFCLVDENG-----YTKKKRNSNFHVLTREETVKEFLSGSNIENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYYKK-INGGLADARNFGLEHAT----GKYIAFVDSDDYIEVAMFERMHDNITEYNADIA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MNDLISVIVPIYNVQDYLDKCINSIINQTYTNLEVILVNDGSTDDSEKICLNYMKNDGRI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73;
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24.7%;
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                        Biosynthesis
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RESULT 13
US-09-767-041-51
; Sequence 51, Application US/09767041
; Patent No. US20020055168A1
                      δÃ
                                                                                                                            ; NAME/KEY: misc_feature
; OTHER INFORMATION: N-terminal part of CPS2J
US-09-767-041-51
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US-09-816-028A-27
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SEQ ID NO 51
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SEQ ID NO 27
LENGTH: 301
TYPE: PRT
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CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: PCT/NL99/0046
PRIOR FILING DATE: 1999-07-19
PRIOR APPLICATION NUMBER: EP98202465.5
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1998-07-22
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SOFTWARE: PatentIn v
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PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
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                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                ORGANISM: Streptococcus
                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                                                                                                                   LENGTH: 120
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                                                                           Local Similarity
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RFDPAYIHAEDYKFWYEAGKLGRLAYYPEALVKYRFHQD 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEKNLGLLRARYEGV----KVANSPYIMFLDPDDYLELNACEECI------- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAMGAW 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith, Hilda
                                                        Conservative
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                                                                                                                                                                                                                                                                      version 3.0
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23.7%;
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                                                                       10.5%;
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                                                                       Score 185.5; DB 1
Pred. No. 2.6e-11;
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                                                       Mismatches
                                                                                        DB 10;
                                                        38;
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                                                        Indels
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(LOS)
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RESULT 15
US-09-765-272-196
; Sequence 196, Application US/09765272
; Patent No. US20020061545A1
; GENERAL INFORMATION:
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; Sequence 39, Application US/09816028A

; Patent No. US2002042369A1
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OTHER INFORMATION: glycosyltransferase from C. jejuni OH4384 (ORF 12a
OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-09-816-028A-39
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SEQ ID NO 39
LENGTH: 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis TITLE OF INVENTION: Gangliosides and Ganglioside Mimics FILE REFERENCE: 019633-000111US CURRENT APPLICATION NUMBER: US/09/816,028A CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: US 60/118,213 PRIOR APPLICATION NUMBER: US 60/118,213 PRIOR FILING DATE: 1999-02-01
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PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FQNEENLGTFASRNLGV----LHSSSDFIMFLDSDDFLTPDACEIAFKEMKKGFDLLC-- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAMG 122
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National Research Council of Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.5%; Score 185.5; DB 10; Length 270; 21.3%; Pred. No. 8.3e-11; ative 48; Mismatches 79; Indels 113;
                                                                                                                                                                                                                          AKCFKKDIILKSFEKIKIDERLNYGEDV----LFCYIYFMFC 195
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                                                          Search completed: December Job time: 7.75447 secs
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                                                                                                                                                                                  298
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                                                                                                                                                                                                                                                                                                                                                186
                                                                                                                                                                                                                                                                                                                                                                                                                              134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85
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TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/961,083 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
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                                                                                                                                          HQLTDTEEYKDICFRLKLFFDAEQR
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                                                                                                                                                                            YSLTDLLDFLTDRVMRKLFAAPQYR
                                                                                                                                                                                                                                                                                                        D---EATMHREYLLASK---IVFINDNLYLYR-
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                                                                                                                                                                                                                                                                                                                                                                                                                            ---KSVLAAIARNGAIWDKPTRHEDIVAVF----PFGNPIHNNTMIMRRSVIDGGLRFD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAMGAWLEVLSEENN------ 133
                                                                                                                                                                                                                          -WARDIVEVFSKKISDCV----
                                                                                                                                                                                                                                                              YWKAAGIAVG----ADCLNYGLLKSTAYALYEKALSGQDIGCLRL----FLYEYFLSLEK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 281 amino acids
TYPE: amino acid
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OPERATING SYSTEM: MSDOS version 6.2
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STATE: Maryland
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Pred. No. 8.7e-11;
3; Mismatches 118;
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Indels

79;

Gaps

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Length 281;

-RRSGSIMRTEFDLS

209

----FSNGRRFD 169

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Minimum I
Maximum I
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No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DB seq length: 2000000000
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1764
1 MQPLVSVLICAYNA
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Match
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	GG GG		0.00	70813 70813 1 transferase A Species: Neisseria m Date: 10-Sep-1999 #s Accession: S70813 Jennings, M.P.; Hood J. Microbiol. 18, 72 Title: Molecular ana Reference number: S7 Accession: S70813 Status: preliminary; Molecule type: DNA Residues: 1-333 <jen (cross-references:="" codon:="" em="" genetics:="" glycosyltr<="" keywords:="" neisser="" note:="" nucleotide="" start="" superfamily:="" td="" the="" ttg=""><td>212.5 211.5 211.5 209 207.5 207.5 207.5 207.5 207.5 207.5 207.5 207.5 207.5 207.5 207.5 207.5 207.5 207.5 207.5 207.5 207.5 209.5 20</td></jen>	212.5 211.5 211.5 209 207.5 207.5 207.5 207.5 207.5 207.5 207.5 207.5 207.5 207.5 207.5 207.5 207.5 207.5 207.5 207.5 207.5 209.5 20
DFLTDRVI DFAADGRI	LREDPAYIHAEDYKFWY :: : LRYNTERDWAEDYQFWY IRAGYWKAAGIAVGADG ::: :::	PRNLGFI	imilarit Conse VSVLICAY	transferase A (EC ss: Neisseria mening 10-Sep-1999 #sequen ion: \$70813 #sequen ion: \$70812 #sequen ion: \$70813	12.0 12.0 12.0 11.8 11.8 11.7 11.7 11.6 11.6 11.5 11.5
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	wwww	AIEKIVGEMEKDRSII 119 	Length 333; Indels 1; Gaps 1; STPAIARHFQEQDGRI 60 :	ngitidis text_change 21-Jul-2000 .; Moxon, E.R. nthesis and phase-variable expres 494 wn; translation not shown wn; translation phase shown EMBL Data Library, April 1995 EMBL Data Library, April 1995	probable glycosylt glycosyl transfera teichuronic acid b glycosyl transfera glucuronosyl transfera glycosyl transfera hypothetical prote beta-1,4-galactosy minor teichoic aci raffinose-raffinos hypothetical prote glycosyl transfera glycosyl transfera glycosyl transfera hypothetical prote glycosyl transfera glycosyl transfera glycosyl transfera glycosyl transfera glycosyl transfera glycosyl transfera

RESULT 2

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A;Gene:
C;Superf
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H81970
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A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R. A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A; Reference number: A81000; MUID:20175755; PMID:10710307
A; Accession: D81027
                                                                        A; Experimental C; Genetics:
                                                                                                                                                                            A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491. A;Reference number: A81775; MUID:20222556; PMID:10761919 A;Accession: H81970
                                                                                                                                                                                                                                    R;Parkhill, J.; Achtman, M.; James, K.D.; Holroyd, S.; Jagels, K.; Leather, S.; McNature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                      lacto-N-neotetraose biosynthesis glycosyl transferase NMA0524 [imported] - Neisseria C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C;Accession: H81970
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C; Superfamily:
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                                                                                       A;Cross-references: GB:AL162753;
A;Experimental source: serogroup
                                                                                                                        A; Molecule type: DNA
A; Residues: 1-346 < PAR>
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A; Residues: 1-349 <TET>
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   Query Match
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                                                     lgtA; NMA0524
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                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAWLDFAADGRMRRLFTLRQYFGILHRLLK 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMGAWLEVLSEEKDGNRLARHHEHGKIWKKPTRHEDIADFFPFGNPIHNNTMIMRRSVID 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RILAQPRNSGLIPSLNIGLDELAKSGGGGEYIARTDADDIAAPDWIEKIVGEMEKDRSII 136
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   58.9%;
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                                                                                       GB:AL157959; NID:g7379120; PIDN:CAB83816.1; PID:g737926
A, strain Z2491
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   Score
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Moule, S.;
   1039;
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Mungall, K.; Quail,
Length 346;
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M.A.;
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Dougherty, B.
Pizza, M.
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Rajandream,
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                                                                                                                            LRFDPAYIHAEDYKFWYEAGKLGRLAYYPEALVKYRFHQDQTSSKYNLQQRRTAWKIKEE
                                                                                                                                                                                                  AWLEVLSEENNKSVLAAIARNGAIWDKPTRHEDIVAVFPFGNPIHNNTMIMRRSVI-DGG
DLIDFLTDRVMRKLFAAPQYRKILKKMLR
                                                                                                         LIFNKDYPYAEDYKFWSEVSRLGCLANYPEALVKYRLHGNQTSSVYNHEQNETAKKIKRE
                                                                                                                                                                                SYLEIIVEK-ECGIIGSQYKTGDIWKNPLLHNDICEAMLFYNPIHNNTMIMRANVYREHK
                                                                    IRAGYWKAAGIAVGADCLNYGLLKSTAYALYEKALSGQDIGCLRLFLYEYFLSLEKYSLT
                                                                                                                                                                                                                                                    ISNKYNLGFINSLNIGLGCFS----GKYFARMDADDIAKPSWIEKIVTYLEKNDHITAMG
                                                                                                                                                                                                                                                                                                                                                                                              151;
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glycosyl transferase homolog HI1578 - Haemophilus influenzae (strain Rd KW20) (;Species: Haemophilus influenzae (c;Species: Haemophilus influenzae (strain c;Species: Haemophilus influenzae (c;Species: Haemophilus influenzae (strain c;Species: Haemophilus influenzae (c;Species: Haemophilus influenzae (c;Species: Haemophilus influenzae (strain c;Species: Haemophilus influenzae (strain c;Specie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-323 <TIGR>
A;Cross-references: GB:U32832; GB:L42023; NID:g1574421; PIDN:AAC23227.1; PID:g1574422
C;Superfamily: Neisseria meningitidis glycosyl transferase A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae FA;Reference number: A64000; MUID:95350630; PMID:7542800 A;Accession: H64130
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ISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAMG
                                                                                                                                                                                           PLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGRIRI
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                                                                                                                         PLVSVIVCAYNAEQYIDESISSIINQTYENLEIIVINDGSTDLTLSHLEEISKLDKRIKI
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5.
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Pred. No. 4.3e-49;
4; Mismatches 107
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5; Mismatches 86;
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M.; Weidman
Jen, N.S.M.
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-INSVSLLEIYHVDKSNK---VLKSILYEMYMSLDKYTIT

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239

179 181 120

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RESULT 6
B97168
glycosyltransferase [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: B97168
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gib
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A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barli
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisi
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: G95948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: G95948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-367 <KUR>
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C; Species: Sinorhizobium meliloti
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                        KYNLQQRRTAWKIKEEIRA------GYWKAAGIAVGADCLNYGLLKSTAYALYEKALS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AWLEVLSEENNKSVLAAIARNGAIWDKPTRHEDIVAVFPFGNPIH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISNPRNIGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAMG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVVSIVLPVYNAEPYIAAAIESVLRQDYERLEVIAIDDGSTDRSRDILERYRKSDSRVSI 63
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                                                                                                                                                                                                                                                                                          AQPGEVRRAYEDGALCFFYFLYQLIAEEEQPRLTH--EFLTRTGKWGLIRRRERYGLLAA 328
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                                                                                                                                                                                                                                                                                                                                        GQ-----DIG--CLRLFLYEYFLSLEKYSLTDLLDFLTDRVMRKLFAAPQYRKILKK 327
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Pred. No. 4.9e-21;
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    Zeng, Q.; Gibson,
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D.H.; Wong, K.
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R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: A97168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glycosyltransferase [imported] - Clostridium acetobutylicum
C;Specias: Clostridium acetobutylicum
C;Specias: 001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: A97168
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A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B97168
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE001437; PIDN:AAK80132.1; PID:g15025168; GSPDB:GN00168 A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-336 < KUR>
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A; Residues: 1-333 < KUR>
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                                               AWLEVLS--EENNKSVLAAIARNGAIWDKPTRHEDIVAVFPFGNPI-HNNTMIMRRSVID 179
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TRIEAFGDIDEKQKTIY----
                                                                                                                             ISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAMG 122
                                                                                                                                                                                                 PKVSIVMPVYNSERYLAEAIESILDQTYNDFEFIIVDDGSTDESYNIISSYANKDNRIIV 64
                                                                                                                                                                                                                              PLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGRIRI 62
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                                                                                              ISR-EHRGLVDSLNEGIN-IAR---GKYTARMDADDISINNRIEKQFEFLELNKDVDILG 119
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28.2%;
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-NSAFSIK-FDSQNIEQVFLTSCAIPHPSVMFKKDSIVK 173
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Pred. No. 8.1e-16;
                                                                                                                                                                                                                                                                                                  Score 263.5; DB 2
Pred. No. 3.1e-14;
1; Mismatches 123
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                                                                                                                                                                                                                                                                                                                                                    336;
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60;

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16;

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A;Cross-references: GB:AE001437; PIDN:AAK80131.1; PID:915025167; GSPDB:GN00168 A;Experimental source: Clostridium acetobutylicum ATCC824 C;Genetics:
                                                                                                                                                  glycosyltransferase [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Date: 197167 C;Accession: H97167 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gib.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001 J. Bacteriol. 183, 4823-4838, 2001 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing: A;Reference number: A96900; MUID:21359325; PMID:21359325
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A;Title: The genes responsible for O-antigen synthesis of Vibrio cholerae O139 are clos A;Reference number: Z22749; MUID:99453293; PMID:10521656
A;Accession: T44330
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C;Species: Vibrio cholerae
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T44330
                                                               A; Molecule type: DNA
A; Residues: 1-333 < KUR>
                                                                                                         A; Reference number: A96900;
A; Accession: H97167
A; Status: preliminary
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C; Superfamily:
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A;Molecule type: DNA
A;Residues: 1-340 <YAM>
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A; Residues: 1-271 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: BH3714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
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Best Local
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                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                               Н
                                                                                                                                                                                                                   MGAWLEVLSEENNKSVLAAIARNGAIWDKPTRHEDIVAVF---PFGNPIHNNTMIMRRSV 177
                                                                                                                                                                                                                                                                                                                                                                                    MQPLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGRI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGIKIKLIDVFKREFKKDFKYIVWGASNGGKITKEVLDEFFEKSQCIAFVDKFKTGEFEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEVLS-----EENNKSVLAAIARNGAIWDKPTRHEDIVAVFPFGNPIHNNTMIMRRSVI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R-ENKGIVYSLNEAI-RLAK---GEYIARMDADDISAPKRIEKQISFLKSHRDIDILGTQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAMGAW 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KMGFAGARRVKAKPIAYIGITV
                                             RTAWKIKEEIRAGYWKAAGIAV
                                                                                                                                                                                                                                                                 RLIHNKNNRGLSYSLAEGV-SLAKA---PWIARMDADDVSFKDRLAVQMDHVKAHSELDI 116
                                                                                                                                                                                                                                                                                                         RIISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 120
                                                                                                                                                                                                                                                                                                                                                    MNPEVTVLMSVYNDKNYLSESIESILNQTFENFEFLIINDASTDGSGELLEEYSKKDKRI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRILHPKDINHIK-FDYVFIATEPGKEEAMSSLKSMGLKCIKDFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---LRELKGYNDFKSEDLDLWLRAIESGFKIYKLKEELIYFRMHEESKTRVDNQNYEGLK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGGLREDPAY -- THAEDYKEWYEAGKLGRLAY-YPEALVKYREHQDQTS--SKYNLQQRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKVVGNISNDIKEKNENKLNI---EFDIYD-DNREKILNYWYCLAHP---
                                                                                     IKAG-SYDRNLRRRQDYDLWFRCLEAKL-KFENIDKPLLYYRSTDDYYKKNNFKVQVQQA
                                                                                                                              IDGGLRFDPAYIHAEDYKFWYEA--GKLGRLAYYPEALVKYRFHQD----QTSSKYNLQQR 232
                                                                                                                                                                           LGSYVIDIDDKGNELEIRKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----KEEIRAGYWKAA-GIAVGADCLNYGLLKSTAYALYEKALSGQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.1%;
26.7%;
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27.5%;
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                                             254
  244
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 249; DB 2;
Pred. No. 3.8e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                           -PTTHKEIANLIWTCPF---IHPTVLFKKDSI 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            108;
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R.;

Masui, N.; Fuji, F.;

C-125)

271;

26;

Gaps

9;

308 331

> 286 279

-SVMFRKDI-

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RESULT 12
AI2091
                                                                                   A;Cross-references: GB:BA000019; PIDN:BAB73987.1; PID:g17131380; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: a112288
                                                                                                                                                                                                                               Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, SDNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana, Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AIZ091
                                                                                                                                                                                                                                                                                          C;Accession: AI2091
C;Accession: AI2091
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, Nakazaki, N.; Shimpo, S.;
                                                                                                                                                                                                                                                                                                                                                                           glucosyltransferase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: FOR996513-997385
C; Keywords: glycosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi. A;Reference number: A64300; MUID:96337999; PMID:86888087
                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-343 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-290 <BUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: H64431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glycosyl transferase (EC 2.4.-.-) - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 10-Oct-1997
C;Accession: H64431
                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:U67549; GB:L77117; NID:g1591709; PID:g1592318; TIGR:MJ1057; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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    Best Local
Matches
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                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMGAWLEVLSEENNKSVLAAIARNGAIWDKPTRH--EDIVAVFPFGNPIHNNTMIMRRSV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRIISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSII 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QPLVSVLICAYN-AEKYFAQSLAAVVGQTWRNLDILI-VDDGSTDGTPAIARHFQEQDGR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPLVSVVMATYNEPEKYLKESIESIXNQTXKDFXFIIXLDNPNNKKAEEIIKEYQQKDKR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILKKLKYDEKLIRSQDYDFWIRCIANDYKFDIIEEFLLKYRIPNRDNYLSRIKKQKLYSY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDGGLREDPAYIHAEDYKEWYEA-GKLGRLAYYPEALVKYRE-HQDQTSSK-----YNL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIFIKNERNLGRGASRN----KAVXIARGKYIAILDADDIALPKRLEKQFKYMENNRDID 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79;
  . Similarity 78; Conserv
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  Conservative
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                        13.9%;
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    50;
Score 244.5; DB Pred. No. 1.2e-150; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 248.5; DB 2; Pred. No. 4.5e-13;
                                         DB 2;
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    Indels
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    53;
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  13;
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Tabata, :
  RESULT 14
AG1920
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C:Genetics:
A.Gene: PAB0772
C;Superfamily: Neisseria meningitidis glycosyl transferase
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A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome A;Reference number: A75001
A;Accession: B75096
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B75096
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C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999
C;Accession: B75096
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A;Residues: 1-298 <KAW>
A;Cross-references: GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB50071.1; PID:g545
A;Experimental source: strain Orsay
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Best Local
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                                                                                      223
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                                                                                                                                                                                                                                                                                                                   119 IAMGAWLEVLSEENNKSVLAAIARNGAIWDK--PTRHEDIVAVFPFGNPIHNNTMIMRRS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 MGGLSA--NVLKQYESWE 232
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nes 83; Conserv
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                                                                                                                                                                                                                                                                                                                                                                   61 YIRLKKNSGGPIARNIGI----KKAKGRFIALLDDDDEWLPHRLEVQVRKFENLGKEFGV 116
                                                                                                                                                                                                                                                                                                                                                                                                              62 IISNPRNLGFTASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEME----KDRSI 118
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                                                                                      LIRK-----HLDIWKNPKI-LSIHLSQMGLLLLLSNNTGKGLKYLTYSIAIAP---
                                                                                                                               TAWKIKEEIRAGYWKAAGIAVGADCLNYGLL-----KSTAYALYEKALSGQDIGCLR 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPIVSVIIPTYNRANLLRRAIASVLNQKFKDFELIVVDDASTDNTPEVVESI--EDGRIR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWI-EKIVGEMEKDRSIIAMGA 123
                                                                                                                                                                            CFKKAGLFDPRLSSSQDWDMWLRIARYYKFDYVDEIIAKYYVHGKQISFNMKKYIPGRER
                                                                                                                                                                                                                          VIDGGLRFDPAYIHAEDYKFWYEAGKLGRLAYYPEALVKYRFHQDQTS---SKYNLQQRR 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HQQNRGLAGARNTGI----RQARGEYLAFVDSDDL----WLPEKLAKHLE------
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LNLENYMI 277
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                                                                                                                                                                                                                                                                        -VSQDGRILGKRLPKHRGDIYSHLLKENFIGSPTLLIRRE 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 243; DB 2;
Pred. No. 1.3e-12,
8; Mismatches 128
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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

Nature 390, 249-256

Nature 390, 249-256

Nature 390,
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG1920
A;Status: preliminary
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: D70036
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A;Residues: 1-337 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB72871.1; PID:g17130260; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYPQQGG-----NHARNRGF-----ELSQ---GEYIQYLDADDYILPEKIEKQVNF 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91;
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Pred. No. 8.9e-12;
il; Mismatches 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:Z99121; GB:AL009126; NID:g2635827; PIDN:CAB15438.1; PID:e11861
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-278 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A69580; MUID:98044033; PMID:9384377 A;Accession: D70036
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Best Local
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                                                                                                                                                                                                                                                     121
                                                                                 203 LYKVREDSDA--FKRRSFTYSID
                                                                                                                                                                                                         180 --GGLRFDPAYIHAEDYKFW---YEAGKLGRLAYYPEALVKYRFHQDQTSSKYNLQQRRT 234
                                                                                                                                                                                                                                                                                             122 GAWLEVLSE--ENNKSVLAAIARNGAIWDKPTRHEDIVAVFPFGNPIHNNTMIMRRSVID 179
                                                                                                                                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                                                                                                                                              62 IISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAM 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                    TLKGYRSVRRTRRMEDIDLWLRFFEEGFRG------
--KLPLSDYI-YIAKPLIRAFMPAAVMNRYHKK 265
                                                                                                                                                                                                                                                     GTGMLVFDEFGVRGARILPSVPEPG-----IMAKGTPFCHGTIMMRASAYR 166
                                       LEKYSLTDLLDFLTDRVMRKLFAAPQYRKILKK 327
                                                                                                                      AWKIKEEIRAGYWKAAGIAYGADCLNYGLLKSTAYALYEKALSGQDIGCLRLFLYEYFLS 294
                                                                                                                                                                                                                                                                                                                                      LIQNKTNKRLAASLNHCLSHAT----GDYIERQDGDDLSFPRRLEKQVAFLEKHRHYQVV 120
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25.2%;
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                                                                                   -ACRRL---
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                                                                                   235
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Search completed: December 2, 2002, 12:00:10 Job time: 15.9563 secs

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Result
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         GenCore version 5.1.3 (c) 1993 - 2002 Compugen Ltd
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YG95_HAEIN
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P22639 anabaena sp
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3 PLVSVLI ::	atch bal s	EMBL; U32832; AAC23227 TIGR; H11578; InterPro; IPR001173; G Pfam; PF00535; Glycos_ Hypothetical protein; 'Complete proteome. SEQUENCE 323 AA; 37	This SWISS-PROT entry is copyright. It is produced th between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no use by non-profit institutions as long as its con modified and this statement is not removed. Usage be entities requires a license agreement (See http://www.or.send.an email to license@lsb-sib.ch).	Venter J.C.; "Whole-genome ran Rd."; Science 269:496-5 -!- SIMILARITY: B	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-Rd / KW20 / ATCC 51907; MEDLINE-95350630; PubMed-7542800; Fleischmann R.D., Adams M.D., White O., Clayton R.A., Ki Fleischmann R.D., Bult C.J., Tomb JF., Dougherty B.A., M Kerlavage A.R., Bult C.J., Tomb JF., Dougherty B.A., Kerlavage A.R., Sutton G., Fitchugh W., Fields C.A., Gocayn McKenney K., Sutton G., Fitchugh W., Fields C.A., Keiley J.M McKenney K., Shirley R., Liu LI., Glodek A., Keiley J.M McKenney K., Hanna M.C., Nguyen D.T., Saudek D.M., Brine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S. Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smit	Haemophilus influen Bacteria; Proteobac Haemophilus. NCBI_TaxID=727;	15-JUL-1998 (Rel 15-JUL-1998 (Rel 15-JUN-2002 (Rel 15-JUN-2002 (Rel Putative glycosy	IN 8_HAEIN		108.5 107.5 107.5 107.7 107 107 108 109 108 108 108 108 108 108 108 108 108 108
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pfam; pF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Complete proteome.
SEQUENCE 290 AA; 35099 MW; 3F6AlB22lC420D74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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30-MAY 27000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update).
Putative glycosyl transferase MJ1057 (EC 2....
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-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
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Q57022; P96336;
15-JUL-1998 (Rel.
15-JUL-1998 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                   EMBL; U32768;
HSSP; P39621;
TIGR; HI0868;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-Rd / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.
Kerney K., Sutton G., Fitzhugh W., Fields C.A., Goodyne J.D.,
Scott J.D., Shirley R., Liu L.-T., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Witterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
Venter J.C.;
                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                         Hypothetical protein; Transferase; Glycosyltransferase; Complete proteome.
SEQUENCE 250 AA; 28915 MW: A5DR220120722700 7777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemophilus influenzae
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                                                                                                         Pfam;
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PF00535; Glycos_transf_2; 1.
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36, Last sequence update)
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               209; DB 1;
No. 3.6e-10;
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63

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Query Match
Best Local Similarity
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                                                                           EMBL; AP003591; BAB74535.1; -.
EMBL; AF031959; AAC32401.1; ALT_INIT.
PIR; B35391; B35391
InterPro; IPR001173; Glycos_transf_2; InterPro; IPR001173; Glycos_transf_2; 1.
PF6am; PF005355; Glycos_transf_2; 1.
                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
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15-JUN-2002 (Rel.
15-JUN-2002 (Rel.
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P22639;
                                                                 Hypothetical protein; Transferase; Glycosyltransferase;
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                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-131 FROM N.A. MEDLINE=90264305; PubMed=2111805; Holland D., Wolk C.P.;
                                                                                                                                                                                                                                                                                                                                                                                                cyanobacterium Anabaena sp. strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      "Identification and characterization of heth, a gene that acts in the process of morphological differentiation of heterocysts. J. Bacteriol. 172:3131-3137(1990).
                                                                                                                                                                                                                                                                                                                                                                                                "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                            Nakazaki N., Shimpo
Yasuda M., Tabata S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=103690;
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                                                                                                                                                                                                                                                                   Bacteriol. 172:3131-3137(1990).
- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
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                                          322
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                                         36388 MW;
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Score 195.5; DB 1 Pred. No. 6.5e-09;
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                                       753C2FB59327D968 CRC64;
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A., Kawashima
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Takazawa M.,
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            Length 322;
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Matches Query Match Best Local

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Q46635;
01-NOV-1997
                                                           Pfam; PF00535; Glycos_trausi_
Exopolysaccharide synthesis;
                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                  use by non-profit institutions as long as modified and this statement is not removed.
                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                         MOI. Microbiol. 15:91/7907(20): 07:- FUNCTION: INVOLVED IN FUNCTIONS OF FUNCTIONS AS A VIRULENCE FACTOR.
                                                                                                                                                                                                                                                                                                                 Bugert P., Gelder K.;
"MoLecular analysis of the ams operon required synthesis of Erwinia amylovora.";
Mol Microbiol. 15:917-933(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
15-JUN-2002 (Rel.
                                               InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Exopollysaccharide synthesis; Transferase; Glycosyltransferase.
SEQUENCE 266 AA; 30748 MW; 163268A4210EB47B CRC64;
                                                                                                             EMBL; X77921; CAA54886.1;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=EA1/79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95319333; PubMed=7596293;
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=552;
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No. 6.7e-09;
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                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X77921; CAA54883.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular analysis of the ams operon required synthesis of Erwinia amylovora."; Mol. Microbiol. 15:917-933(1995).
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SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
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een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
ERYSGL--KINLYLSETKLNGAGARNRGIDLATGDYVCFLDADD----EWHKDKLQQNLS
                                                   PRNLGFIASLNIGLDELAKSGG------
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0535; Glycos_transf_2; 1.
ccharide synthesis; Transferase; Glycos_301 AA; 34788 MW; 99D0EE3080E6EC06
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(Rel. 35, Last sequence update)
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                                                                                                                                                                                                         Conservative
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Pred. No. 1.1e
51; Mismatches
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P11290; P22999;
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01-OCT-1994 (Rel.
16-OCT-2001 (Rel.
                                                                                                 EMBL; U00039; AAB18592.1; -.
EMBL; AE000439; AAC76639.1; -.
EMBL; X06690; CAAC29885.1; -.
PIR; A30268; Q3ECTH.
PIR; B33276; B33276.
ECOGene; EG11266; yibb.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
                                       SEQUENCE
                                                  CONFLICT
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STRAIN=K12 / MG1655;
MEDLINE=94316500; PubMed=8041620;
MEDLINE=94316500; PubMed=8041620;
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"Analysis of the Escherichia coli genome.
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                                                                                                                                                                                                                                                                                                                                                                         dehydrogenase."
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A Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Bouriss R., Bourster L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
A Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
A Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
A Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
A Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
A Gliseppi G., Guy B.J., Haga K., Hajech J., Harwood C.R., Henaut A.,
A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Kurifa K. Landine A. Landine A. Landine S. Landi
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                           Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Prescoan E., Pujic P., Purnelle B., Rapoport G., Reyn M., Reynolds S.
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
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EXOA_RHIME STANDARD; PRT; 330 AA. p33691; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Succincellycan biosynthesis protein exoA (EC 2 EXOA OR RB1082 OR SMB20957.

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InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Transferase; Glycosyltransferase; Complete proteome.
SEQUENCE 446 AA; 53148 MW; BB3698D9B6856C42 CRC6
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non-profit institutions as long
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EMBL; L22636; CAA80345.1; ..
EMBL; AL603645; CAAC49482.1; ..
PIR; S37027; S37027.
PIR; S39956; S39956.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Transferase; Glycosyltransferase; Exopolysaccharide synthesis;
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MEDLINE-94067019; FubMed-8246891;
Becker A., Kleickmann A., Keller M., Arnold W., Puehler A.,
Becker A., Kleickmann A., Keller M., Arnold W., Puehler A.,
"Identification and analysis of the Rhizobium meliloti excAMONP genes
involved in exopolysaccharide biosynthesis and mapping of promoters
located on the exoHKLAMONP fragment.";
Mol. Gen. Genet. 241:367-379(1993).
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                                        ARTDADDIASPGWIEKIVGEMEKDRSIIAMGAWLEVLSEE----NNKSVLAAIARNGAIW 147
                                                                                      NARVVIADGGSTDGTREIARRLATEDPRVLFLDNPKRIQ-SAAVNRAVAEL--GAGSDYL
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pSymB (megaplasmid 2).
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RESULT 10
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Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medique C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi J., Sekowska A., Seror S.J., Serror R., Scoffone F.,
Sekiguchi J., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Vannier F., Vassarotti A.,
Vannier F., Vassarotti A.,
Vannier F., Vassarotti A.,
                                                                                                                                                                                                                                                                                                                                                                                                                               Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guiseppi G., Guy B.J., Haga K., Haiceh J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningsten G., Kroph S., Kumano M.,
                                                                                                         Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Dan
                                                                subtilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., we Presscan E., Santana M., Schneider E., Schweizer J., Ve Rapoport G., Danchin A.;
X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
                                                                         "The complete subtilis.":
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15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WMTDKTSMVYYPRAKLVPLFWQYFGYGRGRAKNFLKHRAMPGLRQMLPLAVAPIAFGALL
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                                            390:249-256(1997)
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                                                                                  of the Gram-positive bacterium Bacillus
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RESULT 11
EXOC_R
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GN EXOC
OOS Rhizob
OOS Rhizob
OOG Plasmi
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OC Rhizob
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RN (1]
RP SEQUEN
RC STRAIN
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                                                                                                                                                      P33697;
01-FEB-1994 (Rel. 28, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                            Succinoglycan biosynthesis protein EXOO OR RB1084 OR SMB20959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDB; 1QG8; 21-APR-00.
PDB; 1QG9; 04-MAY-00.
PDB; 1QG5; 04-MAY-00.
SubtiList; B610609; spsA.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structure of the nucleotide-diphospho-sugar transferase, SpsA fi
Bacillus subtilis, in native and nucleotide-complexed forms.";
Biochemistry 38:6380-6385(1999).

-!- FUNCTION: GLYCOSYLTRANSFERASE IMPLICATED IN THE SYNTHESIS OF
   STRAIN=1021;
MEDLINE=94042869;
                                                                                             Plasmid pSymB (megaplasmid 2)
Bacteria; Proteobacteria; alp
                                                                                                                              Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                  EXOO_RHIME
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                                 SEQUENCE
                                                                  NCBI_TaxID=382;
                                                                                 Rhizobiaceae;
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SIMILARITY: BELONGS
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                                                                                                                                                                                                                                                                                                                                                            ALVKYRFHODOTSSKYNLOORRTAWKIKEEIR
                                                                                                                                                                                                                                                                                                                                                                                            VMHRYSVLEKVKEKFGSYWDESPAFYRIGDARFFWRVNHF--YPFYPLDEELDLNYITDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YQSDISGVKERTEKTRYAALINQAI-EMAE---GEYITYATDDNIYMPDRLLKMVRELDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----IISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEME- 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                   FROM N.A.
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155 243
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                                                                                  Sinorhizobium
                                                                                                                                                                                                                                                  STANDARD;
   PubMed=8226645
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22.1%;
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                                                                                                alpha subdivision;
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Pred. No. 3.
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                                                                                              Rhizobiaceae
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Best Local
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EMBL; Z22636; CAA80347.1; -.
EMBL; Z22636; CAA80347.1; -.
EMBL; Z22636; CAC49484.1; -.
PIR; C49348; C49348.
PIR; C37029; S37029.
PIR; S37029; S37029.
PIR; S39958; S39958.
InterPro; IPROU1173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Transferase; Glycosyltransferase; Exopo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    succinoglycan
J. Bacteriol.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glucksmann M.A., Reuber T.L., Walker G.C "Family of glycosyl transferases needed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS-INSTITUTE of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vorhoelter F.J., Hernandez-Lucas I.,
Golding B., Puehler A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21396508; PubMed=11481431; Finan T.M., Weidner S., Wong K., B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=RCR2011 / SU47;
MEDLINE=94067019; PubMed=8246891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fixing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: GLYCOSYLTRANSFERASE REQUIRED FOR THE SYNTHESIS OF SUCCINOGLYCAN (EPS I). NEEDED FOR THE ADDITION OF THE FIFTH (GLUCOSE), CATALYZES THE FORMATION OF A BETA-1,6 LINKAGE BET THE FOURTH AND FIFTH SUGAR.
PATHWAY: Exopolysaccharide biosynthesis.
SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAUTION: Ref.1 sequence differs from that frameshift in position 208\,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete sequence of the 1,683-kb pSymB megaplasmid ng endosymbiont Sinorhizobium meliloti.";
. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
                                                 TMIMRRSVIDGGLRFDPAYIHAEDYKFWYEAGKL-GRLAYYPEALVKYRFHQDQTS 224
                                                                                                  NLDVVSLDGRSLRMFSEAELARLPQLTLPAFIESNVLF--RSEHN-----FGYMKPIFE-
                                                                                                                                                                                                                                                                                                                                                                PLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGRIRI
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                                                                                                                                                                                                       IALDRNRGPGGARNAGIG----AARGRWIAVLDSDDTVRPDRLRRMIERADAAGAQIAVD
                                                                                                                                                                                                                                                           ISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIAM- 121
                                                                                                                                                                                                                                                                                                                  PDVTFVVAAYNSADTIVRAIESALAQEGVTVEVVVVDDCSADATPALVAAI--PDPRVRL
                                                                                                                                                                                                                                                                                                                                                                                                                         60;
                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 25.4
50; Conservative
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RRFLENQQLRFDEALRIGEDYILLASALACGGRCAVEPSAGYIYHIREGSIS 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genet. 241:367-379(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the exoHKLAMONP fragment.";
                                                                                                                                                      -GAWLEVLSEEN----NKSVLAAIARNGAIWDKPTRHEDIVAVFPFGNPIHNN
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175:7033-7044(1993).
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25.4%;
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; 770B43782F785579
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
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I., Becker
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                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
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Cowie
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                                                                                                                                                                                                                                                                                                                                                                                                                       32;
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RESULT 12
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Best Local
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01-NOV-1997
01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                    "A 718-kb DNA sequence of the Esche corresponding to the 12.7-28.0 min DNA Res. 3:137-155(1996).
-!- SUBCELJULAR LOCATION: Integral
-!- SIMILARITY: TO Y.PESTIS HMS LOC S.EPIDERMIDIS ICAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                              entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97426617; PubMed=9278503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mau B., Shao Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YCDQ_ECOLI
                                                                                                                                                                                                                                  [nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
ISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADD-----IASPGWIEKIVGEME 113
                          PSISIIIPCFNEEKNVEETIHAALAQRYENIEVIAVNDGSTDKTRAILDRMAAQIPHLRV 134
                                                  PLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGRIRI 62
                                                                                                                                                                                                                                                          AE000204; AAC74107.1; -. D90739; BAA35803.1; -.
                                                                                                                                                                                                      PF00535; Glycos_transf_2; 1.
netical protein; Transmembrane;
                                                                                        Similarity
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
                                                                             Conservative
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hes 108;
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RESULT 13
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                                                                                Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yasuhoto K., Yashida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchi
                                                                                                                                                                                                                                                                                     Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Vanier F., Vassarotti A., Vanier P., Tognoni M., Vanier F., Vassarotti A., Vanier P., Vass
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Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.
Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,
Rapoport G., Danchin A.;
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Best Local (
                                                 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E., III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Stalton J.E., Taylor K., Whitehead S., Barrell B.G.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from complete genome sequence."; Nature 393:537-544(1998).
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01-NOV-1997 (Rel. 35, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Hypothetical protein Rv1520.
RV1520 OR MT1570 OR MTCY19G5.08C.
Mycobacterium tuberculosis.
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                                                                                                                                                                                         MEDLINE=98295987; PubMed=9634230;
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InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
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EMBL; Z99123; CAB15824.1;
PIR; S39711; S39711.
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                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.3%;
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Pred. No. 5.2e-05;
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Matches 60
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequ
15-JUN-2002 (Rel. 41, Last ann
           McLaughlin R., Abu
                                                     SEQUENCE FROM
                                                                                                          Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 346 AA; 39578 MW; 22EDA40495E0EFCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                        STRAIN=A2;
                                                                               NCBI_TaxID=727;
                                                                                                                                       HI1695
                                                                                                                                                 Putative glycosyl transferase HI1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR; MT1570;
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                                                                                                                        Haemophilus influenzae
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SEQUENCE FROM N.A.
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AE007024; AAK45837.1; ALT_INIT
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        Young R., Spinola S., Apicella
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Pred. No. 0.00019;
                                                                                                          subdivision;
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                                                                                                                                               update) (EC 2.-.-).
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Pfam; PF00535; Glycos_transf_2; 1.

Hypothetical protein; Transferase; Glycosyltransferase;

Complete proteome.

COMPLICT 26 26 V -> G (IN REF. 1).

CONFLICT 46 46 D -> E (IN REF. 1).

CONFLICT 49 49 F -> S (IN REF. 1).

CONFLICT 49 49 F -> S (IN REF. 1).
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Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 269:496-512(1995).
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M94855; AAA24983.1; -. EMBL; U32842; AAC23341.1; -. TIGR; HI1695; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Whole-genome random sequencing and assembly of Haemophilus influenzae {\tt Rd.}";
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STRAIN-Rd / KW20 / ATCC 51907;
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                                                                                                                     KEEIRAG
                                                                                                                                                                                          GLRFDPAYIHAEDYKFWYEAGKLG-RLAYYPEALVKYRFHQDQTSSKYNLQQRRTAWKI- 238
                                                                                                                                                                                                                                      GGQIAEFGKNVNDIV-----
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                                                                                                                                                                                                                                                                                                               LVKLPQNRGLGKALNEGLLHC----DYDWVFRMDTDDICVPDRFEKQVAFIEQHPESIIF 117
                                                                                                                                                                                                                                                                                                                                                                                            SVLMSLYIKENPQFLRECFESLVAQTRQADEIVLVFDGVV--TPDLEFVVTEFETKLPLK 61
                                                                                                                                                         GGYED----LQEDYYLWIKLVAQGLYMANLPDILVYARVGNGMYSRRRGVNQAKAEWRLF 225
                                                                                                                                                                                                                                                                                                                                                                                                                                 SVLICAYNAE -- KYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGR--IR 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 8.0%; Score 140.5; DB 1; Length 267; l Similarity 25.5%; Pred. No. 0.00018; 63; Conservative 45; Mismatches 114; Indels 25
                                                                               232
                                                                                                                     245
                  2
                    2002, 11:56:29
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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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   SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_invertebr:
6: sp_mammal:*
7: sp_mhc:*
10: sp_plant:*
11: sp_rodent:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebr:
14: sp_unclass:
15: sp_archeap:
16: sp_bacterii
17: sp_archeap:
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1764
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Gapop 10.0 , Gapext 0.5
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sp_phage:*
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sp_bacteria:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

110 110 110 1110 1110 1110 1110 1110 1	Result
1074.5 1069.5 1069.5 1049.5 1049 1048 1048 1045 1045 103 942.5 712.5 743.3 443.3	Score
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221							225											249	258	258.5	63.5	65.5	272	275	282.5	30.5	346	
12.5		12.6	•			•	12.8				•		•			13.8		14.1	14.6	٠	٠		15.4			18.7	9	
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16	N	16	16	2	16	17	16	16	16	17	16	16	N				16	16	16	N	16	2	Ν	Ν	16	16	16	N
P71057	Q8VLB0	Q8YW50	Q8YSM2	082874	Q9K6S0	058167	Q8YSL3	Q8YSL4	Q97P78	Q8U2R3	P71054	Q8YYD6	Q93CQ9	Q9K2R3	Q56869	Q9UZI6	Q8YUP7	Q9K6L5	Q97H40	087159	Q97н39	Q9LA88	Q93EK8	P96944	Q97Н38	Q98ЛН2	Q92V61	P74947
P71057 bacillus su			Q8ysm2 anabaena sp	082874 streptococc		O58167 pyrococcus			-	Q8u2r3 pyrococcus	P71054 bacillus su	σ	Q93cq9 shigella bo	Q9k2r3 neisseria g	Q56869 yersinia en		Q8yup7 anabaena sp	Q9k615 bacillus ha	Q97h40 clostridium	087159 vibrio chol	Q97h39 clostridium	Q91a88 aeromonas h	Q93ek8 neisseria m	P96944 neisseria m	Q97h38 clostridium		Q92v61 rhizobium m	P74947 vibrio chol

ALIGNMENTS

Qy	Db	Qy	Db	Qy	X m o	QS	KW	DR	DR	DR	RL	RT	RT	RA	RX	RC	RP	RN	οx	8	SO	GN	DE	DΤ	TO	DT	AC	ID	Q50949	RESULT	
121 MGAWLEVLSEENNKSVLAAIARNGAIWDKPTRHEDIVAVFPFGNPIHNNTMIMRRSVIDG 180	61 RIISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 120	61 RIISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 120	1 MQPLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGRI 60	1 MQPLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGRI 60	Query Match 100.0%; Score 1764; DB 2; Length 337; Best Local Similarity 100.0%; Pred. No. 4.8e-137; Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE 337 AA; 38393 MW; 5AE21AA75CAA732E CRC64;	Transferase.	Pfam; PF00535; Glycos_transf_2; 1.	InterPro; IPR001173; Glycos_transf_2.	EMBL: U14554: AAA68012.1:	J. Exp. Med. 180:2181-2190(1994).	ide.";	"Genetic locus for the biosynthesis of the variable portion of	Gotschlich E.C.;	MEDLINE=95053752; PubMed=7964493; ·	STRAIN=F62;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=485;		Neisseria gonorrhoeae.	LGTD.		1. 17, Last	(TrEMBLrel. 01,	-1996 (TrEMBLrel.	Q50949; ·	Q50949 PRELIMINARY; PRT; 337 AA.	949	ULT 1	

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Best Local Sim
Matches 218;
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Q9EVD5;
01-MAR-2001 (TIEMBLIEL 1
01-MAR-2001 (TIEMBLIEL 1
01-JUN-2002 (TIEMBLIEL 2
                               Q51115
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Arking D., Tong Y., Stein D.C.;
"Analysis of lipooligosaccharide biosynthesis
J. Bacteriol. 183:934-941(2001).
EMBL; AF240672; AAG09764.1; -.
HSSP; P39621; 10GQ.
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Bacteria; Proteobacteria;
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PF00535; Glycos_transf_2; 1.
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Query Match
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Matches 218
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Q9JXQ6;
01-OCT-2000
01-OCT-2000
01-DEC-2001
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Bacteria;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., N
Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J
Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.
Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dough
Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96414473; PubMed=8817494; Jennings M.P., Hood D., Peak I.R.A., Virji M., Moxon E.R.; Jennings M.P., Hood D., Peak I.R.A., Virji M., Moxon E.R.; "Molecular analysis of a locus for the biosynthesis and phase-var: expression of the lacto-N-neotetraose terminal lipopolysaccharide expression of the lacto-N-neotetraose terminal lipopolysaccharide structure in Neisseria meningitidis.";
                                                                                                      SEQUENCE FROM N.A.
STRAIN-MC58 / SEROGROUP B;
MEDLINE-20175755; PubMed-10710307;
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Bacteria; Proteobacteria;
NCBI_TaxID=487;
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01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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EMBL; U25839; AAC44084.1;
                                                                                                                                                                                             NCBI_TaxID=491;
                                                                                                                                                                                                                                                                              Lacto-N-neotetraose
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Proteobacteria; beta subdivision;
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
tetraose biosynthesis glycosyl transferase
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65.9%;
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Last sequence update)
Last annotation updat
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9; Mismatches
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Best Local S
Matches 212
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Best Local S
Matches 217
                                                                                                                                                 "Characterization of lipooligosaccharide gonorrhoeae PID2.";
                                                                                                       Submitted (OCT-2000) to the EMBL/GenBank/DDBJ EMBL; AF313394; AAK70338.1; . InterPro; IPR001173; Glycos transf_2. Pf4mg, PF00535; Glycos_transf_2; 1.
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01-MAR-2002
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Pfam; PF00535; Glycos_transf_2; 1.
Transferase; Complete proteome.
SEQUENCE 349 AA; 40618 MW; 4B9E24
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EMBL; AE002541; AAF42258.1;
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                                                                                                 Transferase
                                                                                                                                                                                                                                        Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta
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MQPLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGRI 60
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Last annotation updat
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                                  Score 1055; DB 2;
Pred. No. 1.2e-78;
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Pred. No. 7.56
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Q50946;
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-JUN-2001 (TrEMBLrel. 1
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J Exp. Med. 180:2181-2190(1994).
EMBL; U14554; AAA88009.1;
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Bacteria; Proteobacteria;
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241
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                                                                                                                                                           RIISNPRNLGFIASLNIGLDELAKS--GGGEYIARTDADDIASPGWIEKIVGEMEKDRSI 118
                                                                                                                                                                                                        MOPLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTDGTPAIARHFQEQDGRI
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                      KEEIRAGYWKAAGIAVGADCLNYGLLKSTAYALYEKALSGQDIGCLRLFLYEYFLSLEKY
                                                             DGGLRFDPAYIHAEDYKFWYEAGKLGRLAYYPEALVKYRFHQDQTSSKYNLQQRRTAWKI 238
                                                                                                                                             KILAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSI
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Pred. No. 3.
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Harvey H.A., Porat N., Campbell C.A., Je
Phillips N.J., Apicella M.A., Balke M.S.
"Gonococcal lipooligosaccharide is a lig
receptor on human sperm.";
Mol. Microbiol. 36:1059-1070(2000).
EMBL; AF121135; AAF14359.1; -
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
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    NCBI_TaxID=485;
                        Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
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Nelsseria meningitidis (serogroup A).
Bacteria, Proteobacteria; beta subdivision: Naisonal NCBI_TaxID=65699.
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EMBL; U15992; AAA92074.1; -.

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STRAIN-96099316; PubMed-8522539;
                                  Naturé 404:502-506(2000).

EMBL; AL162753; CAB83816.1; -.

InterPro; IPR001173; Glycos_transf_2.

pfam; PF00535; Glycos_transf_2; 1.
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MEDLINE=20222556; PubMed=10761919;
MEDLINE=20222556; PubMed=10761919;
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MEDLINE=2022256; PubMed=10761919;
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Stein D.C.;
                                                                                                                                                                                              Whitehead S., Spratt B.G., Barrell B.G.; "Complete DNA sequence of a serogroup A
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF708059; AAF75877.1;
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
SEQUENCE 321 AA; 37052 MW; 6ACADA9A3CB738FA CRC64;
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01-JUN-2001
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Bacteria; Proteobacteria;
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                                                                                                            IWDKPTRHEDIVAVFPFGNPIHNNTMIMRRSVIDGGLRFDPAYIHAEDYKFWYEAGKLGR 205
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                                                                                                                                                                           GGGEYTARTDADDIASPGWIEKIVGEMEKDRSITAMGAWLEILSEEKDGNRLARHHRHGA
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                                                                                 IWDKPTRHEDIAAFFPFGNPIHNNTMIMRRSVIDGGLRYDTGRDWAEDYQFWYDVSKLGR
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                                                                                                                                                                                                                                                                                                                                                               Score 953; DB 2;
Pred. No. 2.6e-70;
4; Mismatches 80
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Pred. No. 2.4e-77;
5; Mismatches 86;
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 321;
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Q9189

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         RESULT 12
Q9CLR9
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Q9L8F0;
01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
NCBI_TaxID-485;
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                                                                                                                                                                                                                                                                                                                   LKKMLR 330
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influence serum-resistance
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                                                                                                                                                     PRT;
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Matches 156
Query Match
Best Local Similarity
Matches 121; Conserv
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Q93EK6;
Q1-DEC-2001
Q1-DEC-2001
Q1-DEC-2001
                                                                                                                     Zhu P., Klutch M.J., Tsai C.-M.; "Genetic Analysis of Conservation and Variation of Lipooligosaccharide Expression in Two L8-Immunotype Strains of Neisseria meningitidis."; FEMS Microbiol. Lett. 203:173-177(2001).

EMBL: AF355193; AAL12840.1; -.
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                             Neisseria;
Bacteria;
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                                                                                                                                                                                                                                          MEDLINE=21467954; PubMed=11583844;
                                                                                                                                                                                                                                                                   STRAIN-M978
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=487;
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Pfam; PF00535; Glycos_transf_2; 1.
PF00535; Glycos_transf_2; 1.
SEQUENCE 337 AA; 39267 MW; 8639BCFB5F700DB4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLRFDPAYIHAEDYKFWYEAGKLGRLAYYPEALVKYRFHQDQTSSKYNLQQRRTAWKIKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAINYYLQDLGVIHRLGEDIFFHDIETIQAEL---ASLSLLDNCIIKRILYDCYLSLVDN
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Proteobacteria;
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    Conservative
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55.3%;
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Pred. No. 1.7e-
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Pred. No. 1.7e-40;
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P96946;
01-MAY-1997
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01-JUN-2002
                                                   Neisseria
Bacteria;
                                                                                     Glycosyl transferase.
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Transferase.
172 AA;
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EMBL; AF121135; AAF14362.1; -.
EMBL; AF121135; Glycos_transf_2.
FinterPro; IPR001173; Glycos_transf_2.
FinterPro; Glycos_transf_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20305049; PubMed=10844691;
Harvey H.A., Porat N., Campbell C.A., Jennings M.,
Phillips N.J., Apicella M.A., Balke M.S.;
"Gonococcal lipooligosaccharide is a ligand for the
"eceptor on human sperm.";
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Bacteria;
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STRAIN=126E;
MEDLINE=20055626;
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                                       NCBI_TaxID=487;
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RA Jennings M.P., Srikhanta Y.N., Moxon E.R., Kramer M., Poolman J.T.,
RA Kuipers B., van der Ley P.;
RT "The genetic basis of the phase variation repertoire of
RT lipopolysaccharide immunotypes in Neisseria meningitidis.";
RT Microbiology 145:3013-3021(1999).

RL Microbiology 145:3013-3021(1999).

RL Microbiology 145:3013-3021(1999).

RL Microbiology 145:3013-3021(1999).

REMBL; U65788; AAB48386.1; -.

DR EMBL; U65788; AAB48386.1; -.

DR FIGHT PF00535; Glycos_transf_2: 1.

PF00535; Glycos_transf_2: 1.

RKW Transferase.

SQ SEQUENCE 149 AA; 16867 MW; 68A52EB7DF6B552A CRC64;

Query Match
SEQUENCE 149 AA; 16867 MW; 68A52EB7DF6B552A CRC64;

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Human polypeptide
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Novel human secre	AAU30597	22	439		85	43
Listeria monocytoq	ABB47763	23	653		85.5	42
Human protein sequ	AAB92861	22	526	•	86	41
Listeria monocytog	ABB49964	23	291		86	40
	AAW81169	19	1674		87	39
Novel human secre	AAU33259	22	1343		87.5	38
Bovine differentia	AAW77286	19	1129	•	87.5	37
Staphylococcus	AAU36547	22	662	6.1	87.5	36
Amino acid	AAB08632	21	662	•	87.5	35
Staphylococcus	AAU33784	22	657		87.5	34
Worm C38H2-2/141-	AAE15943	23	161		88.5	33
Black widow	AAR80097	16	1214		90.5	32
Black widow spider	AAR80096	16	991	•	90.5	31
Caenorhabditis ele	AAB82459	22	389		91	30
Drosophila	ABB61520	22	4010		94	29
Novel human diagno	ABG11534	22	767	•	94	28
H. pylori beta-1,4	AAY32543	20	273		95	27
Helicobacter pylor	AAU76669	23	444	•	97	26
Helicoba	AAB60321	22	273		97	25
	AAW24257	18	394		99	24
H. pylori cytopla	AAW21023	18	279	7.2	103	23
	AAB60317	22	273		104	22
H. pylori cytoplas	AAW20604	18	201		106.5	21
Novel human diagno	ABG22090	22	168		108.5	20
	ABB11417	22	739	•	109	19
	ABP43477	23	622		127	18
	AAB88452	22	622		127	17
	AAM93427	22	622		127	16
	AAB41900	21	521	•	127	15
Human ovarian ant	ABP42016	23	636	٠	129.5	14
Hydrophobic domain	AAB12121	21	595		129.5	13
	308	20	579		129.5	12
Human AFP	AAG81257	22	578	9.0	29.	11

ALIGNMENTS

KESULT 1 AAR91315

AAR91315 standard; Protein; 280

09-JUL-1996

(first entry)

N. gonorrhoeae glycosyltransferase LgtE.

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Nucleic acids encoding glycosyl transferase(s) diagnosis of infection with Neisseria and for oligo:saccharide(s)
                                                                                                                                                                 Glycosyltransferase; lipo-oligosaccharide;
                              N-PSDB; AAT14061
                                     WPI; 1996-200924/20
                                                    Gotschlich
                                                                                                               04-APR-1996
                                                                                                                              WO9610086-A1
                                                                                  26-SEP-1994;
                                                                                               25-SEP-1995;
                                                                                                                                           Neisseria gonorrhoeae
                                                                 (UYRQ ) UNIV
                                                                   ROCKEFELLER.
                                                                                 94US-0312387
                                                                                               95WO-US12317
                                                                                                                                             strain F62
                                                                                                                                                                lgt gene; LOS locus;
       ) - used in the the biosynthesis
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AAWO6580

ID AAWO
XX
AC AAWO
AC AAWO
AC AAWO
DT 21-y
XX
VX
PO13
KW PO13
KW N-ac
XX
Ne11
XX
VO96
PD 19-1
PF 03-,
XX
PP 03-,
XX
PR 07-,
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PR 08-,
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PR WPI
DR WP
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Best Local S
Matches 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 Glycosyltransferases (AAR91311-15) are products of the lgt locus (AAT14061) of Neiserria gonorrhoeae strain F62. Glycosyltransferase LgtE (AAR91315) can be obtd. by expression of the lgtE coding sequence in recombinant host cells. A method for adding Gal betal-4 to GlcNac or Glc comprises contacting a reaction mixture contg. activated Gal to an acceptor moiety comprising a GlcNac or Glc residue in the presence of LgtE. Oligosaccharides can be produced that, when attached to non-toxic lipids, are useful for Neisseria vaccine prepn. Blood group core oligosaccharides, and mimics of lacto-N-neotetraose, gangliosides and saccharide portions of globoglycolipids can also be produced using the enzymes.
     Transfer of at least
                                                                                                                                                                                                                                                    07-JUN-1995;
                                                                                                                                                                                                                                                                                                          03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                19-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                      WO9640971-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria gonorrhoeae ATCC 33084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polyglycosyltransferase; N-acetylglucosaminyl transferase; N-acetylgalactosaminyl transferase; lipo-oligosaccharide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW06580 standard; Protein;
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                                                           AAT49230
                                                                                                                                                                                              NEOSE TECHNOLOGIES
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                                                                                                                                           Johnson
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     saccharide units
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Pred. No. 6.4e-148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
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using
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RESULT 3
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Best Local S
Matches 278
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         Nucleic acids encoding glycosyl transferase(s) diagnosis of infection with Neisseria and for
                                                  WPI; 1996-200924/20
P-PSDB; AAT14061.
                                                                                                                                                                           25-SEP-1995;
                                                                                                                                                                                                      04-APR-1996
                                                                                                                                                                                                                                                          Neisseria gonorrhoeae strain F62
                                                                                                                                                                                                                                                                                                 Glycosyltransferase; lipo-oligosaccharide;
                                                                                                                                                                                                                                                                                                                                                         09-JUL-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             AAR91312 standard; Protein; 279
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                                                                                                                     (UYRQ ) UNIV
                                                                                                                                                 26-SEP-1994;
                                                                                                                                                                                                                                WO9610086-A1
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278; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                      ROCKEFELLER
                                                                                                                                                94US-0312387
                                                                                                                                                                           95WO-US12317.
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99.3%;
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Pred. No. 2.7e-146;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                 lgt gene; LOS locus;
         ) - used in the the biosynthesis
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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
WPI;
                                                                                                                                                                                                                                          glycosyltransferase; accessory enzyme; nucle saccharide donor; oligosaccharide synthesis; carbohydrate structure development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria vaccine prepn. Blood group core oligosaccharides, and mimics of lacto-N-neotetraose, gangliosides and saccharide portions of globoglycolipids can also be produced using the enzymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence in recombinant host cells. A method for adding Gal betal-4 to GlcNAc or Glc comprises contacting a reaction mixture conty, activated Gal to an acceptor moiety comprising a GlcNAc or Glc residue in the presence of LgtB. Oligosaccharides can be produced that, when attached to non-toxic lipids, are useful for the presence of LgtB.
                           Gilbert M,
                                                                                    14-DEC-1998;
15-DEC-1997;
                                                                                                                                                          24-JUN-1999
                                                                                                                                                                                       W09931224-A2
                                                                                                                                                                                                                Neisseria meningitidis
                                                                                                                                                                                                                                                                                      Beta-1,4-galactosyltransferase; lgtB; fusion protein; catalytic domain;
                                                                                                                                                                                                                                                                                                                   N. meningitidis Beta-1,4-galactosyltransferase
                                                                                                                                                                                                                                                                                                                                                 08-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                       AAY22156 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 Glycosyltransferases (AAR91311-15) are products of the 1gt locus (AAR14061) of Neiserria gonorrhoeae strain F62. Glycosyltransferase
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                                                                                                                             15-DEC-1998;
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1999-395174/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LETMFAKVIVRPDKVLNYENRSFPLLESEHCGTAGYIISREAMRFFLDRFAVLPPERIKA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDLMMFTYFFDKEGMPYYQVSPALCTQELHYAKFLSQNSMLGSDLEKDREQGR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VDLMMFGNPDDREGMPVCQLNPALCAQELHYAKFHDQNSALGSLIEHDRRLNRKQQWRDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al Similarity
209; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Fig
                                                       NAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279
                            Wakarchuk WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                      RES COUNCIL CANADA
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                   98US-0211691.
97US-0069443.
                                                                                                                             98WO-CA01180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.0%;
71.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LIRALTKIGREREKRRQRR-----EQLIGKIIVPFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1036.5; DB 1
Pred. No. 4.7e-104;
                            ZM.
                                                                                                                                                                                                                                                                          nucleotide sugar formation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17; Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279
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RESULT 5
AAW89331
ID AAW8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The fusion proteins are able to catalyse more than one reaction involved in the enzymatic synthesis. This is useful for the development of therapeutic agents that have specific carbohydrate structures. Carbohydrates are involved in recognition elements on the surface of cells. The fusion protein can be used for the synthesis of both natural carbohydrates and synthetic derivatives with novel properties. The fusion protein carbohydrates and synthetic derivatives with novel properties. The fusion polypeptide allows two glycosyltransferase reactions in a single vessel, provides improved yields of end products. Additionally, cleanup and disposal of extra solvents and by-products is reduced. The fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    galactosyltransferase (also referred to as lgtB). The invention relates to a nucleic acid encoding a fusion protein that comprises a glycosyltransferase catalytic domain and a catalytic domain from an accessory enzyme that is involved in formation of a nucleotide sugar which is a saccharide domor for a glycosyltransferase reaction. The fusion protein is useful in the enzymatic synthesis of oligosaccharides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A new glycosyltransferase fusion synthesis of oligosaccharides
                                                                                                                                     Neisseria meningitidis; lgtC; lgtB; beta-1,4-galactosyltransferase; glycosyltransferase; proteolytic enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the Neisseria meningitidis Beta-1,4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAX84281.
                                                                   WO9854331-A2
                                                                                                    Neisseria meningitidis
                                                                                                                                                                                      Neisseria meningitidis lgtE C-terminal peptide
                                                                                                                                                                                                                           26-FEB-1999
                                                                                                                                                                                                                                                                                                AAW89331 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with a terminal galactose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Fig 2;
                                                                                                                                                                                                                                                                                                                                                                                      241
                                                                                                                                                                                                                                                                                                                                                                                                                       237
                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MQNHVISLASAAERRAHIADTFGSRGIPFQFFDALMPSERLEQAMAELVPGLSAHPYLSG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              also use directly different donor analogues and various acceptors 
h a terminal galactose residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VDLMMFTYFFDKEGMPVYQVSPALCTQELHYAKFLSQNSMLGSDLEKD----REQGRRHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PANTFKHRLIRALTKISREREKRRQRREQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LETMFAKVIVRPDKVLNYENRSFPLLESEHCGTAGYIISREAMRFFLDRFAVLPPERIKA 180
                                                                                                                                                                                                                                                                                                                                                                                                                     RSLKVMFDLKRALGKFGREKKKRMERQRQ 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDLMMFSDFFDREGMPVCQLNPALCAQELHYAKFHDQNSALGSLIEHDRLLNRKQQRRDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LETMFMHVLTSPSGVADYCGRAFPLLESEHWGTAGYIISRKAMRFFLDRFAALPPEGLHP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MQNHVISLASAAERRAHIADTFGRHGIPFQFFDALMPSERLEQAMAELVPGLSAHPYLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63pp; English
                                                                                                                                                                                                                                                                                            peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.98;
74.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1007; DB 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein useful in the enzymatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.5e-101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
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26-MAY-1998; 03-DEC-1998.

98WO-IB00975

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ABB62795
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A method has been developed of expressing a glycosyltransferase in a host cell. The method comprises introducing into the host cell a nucleic acid encoding the glycosyltransferase and incubating the host cell under conditions appropriate for expression of the glycosyltransferase, where the host cell substantially lacks a protease that cleaves polypeptides between two consecutive positively charged amino acid residues. The glycosyltransferase can be used in in vitro production of oligosaccharide structures which are potential therapeutic agents for use in the manipulation of cell-cell recognition events, particularly adhesion of bacteria and viruses to mammalian cells and leukocytended and cell interaction through selectins in inflammation. The
              N-PSDB; ABL06898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     method provides more readily recoverable active glycosyltransferases than prior art methods involving mammalian glycosyltransferases. The present sequence represents a C-terminal peptide from Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expressing high levels of glycosyltransferases - comprises use either host cells deficient in proteolytic enzymes or modified glycosyltransferase genes deleted in a proteolytic recognition
                            WPI; 2001-656860/75
                                                                                                               23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                              Drosophila melanogaster
                                                                                                                                                                                                                                                                                          Drosophila;
                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       meningitidis lgtE from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAY-1997;
                                                                                                                                                         23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                   WO200171042-A2
                                                                                                                                                                                                                                                                           pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                            ABB62795
                                                                                                                                                                                                                                                                                                                                                                                                         ABB62795 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig
                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 QGRRHRRSLKVMFDLKRALGKFGREKKKRMERQRQAELEKVYGRRVILFK 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QERRHRRSLKVMFDLKRALGKFGREKKKRMERQRQAELEKAYGRRVISFK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1999-035177/03.
                                                       JC,
                                                                                     PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 AA;
                                                     Adams M,
                                                                                                                                                                                                                                                                                        developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RES COUNCIL CANADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Young NM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0047751.
                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.2%;
                                                       Ľ
                                                       PWD,
                                                                                                                                                                                                                                                                                                                                                                                                         1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 233; DB Pred. No. 9.4e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                       Myers
                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233; DB 20;
No. 9.4e-18;
                                                       EW;
                                                                                                                                                                                                                                                                                                                   ID NO 15177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                   1119
                                                                                                                                                                    Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antilocervulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511) and the encoded proteins
                                                                                                                                       cardiant; gene therap
neurological disease;
                                                                                                                                                                                                                                    Human polypeptide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                      ABB89453 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1059
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specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cel
                                                                           WO200190304-A2
                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                       24-MAY-2002
                                                                                                                                                                                                                                                                                                      ABB89453;
                                            29-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                               247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                 ESLSKSHQE 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLGYVISLQGA----LKLLAAKPLDKLIPVDEFLPLMFDRHPNKTWTEAFPKRNLVAFSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MINLKRRPERREKMERLFDEIGIEAEHFPAVDGKELSTERLLEMGVRFLPGYEDPYHHRA 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VISLASAAERRAHIADTFGSRGIPFQFFDAL----MPSERLEQAMAELVPGLS----AHPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RALGKFGRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLLLYPIYYTGESGYISDTEDSQQISVETSEEGEARLKSDREQVFDHEQEFKLNPELKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PALC----TQELHYAKFLSQNSMLGSD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAGYIISREAMRFFLDRFAVLPPERIKAVD----LMM-----FTYFFDKEGMPVYQVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVRLETMFAKVIVRPDKVLN------YENRSFPLLESE----HCG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSGVEKACFMSHAVLWEQALDEGLPYIAVFEDDVLLGEGAEQFLAEDTWLEERFDKDSAF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -IRFEPYFRQNAVR---ILNQARNAAQYDLIYFGRKRLKEESEPAVENADNLVHAGYSYW 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MTMGEIGCFLSHYNIWVMWVRKQLKEVLILEDD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                        therapy; cancer; immune
isease; infection; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ata for this patent did not form part of the printed but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID NO 15177;
                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
                                                                                                                                                                                                                                                                                                                                      423
                                                                                                                                                                                                                                        1829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 144; DB 22;
Pred. No. 3.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                         immune disorder;
                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LEKDREQGRRHRRSLKVMFDLK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid detection reagent
                                                                                                                                                         cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92;
                                                                                                                                                                                     antiulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                         disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152
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18-MAY-2001; 2001WO-US16450

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                                                                                                                                                                                                                                   AAB41790
                                                                                                                                                                                                                                                      RESULT 8
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease, multiple sclerosis, rheumatoid arthritis and ulcerative colifitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breas and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn
                          Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant
                                                                                                    Human ORFX ORF1554 polypeptide sequence SEQ ID NO:3108
                                                                                                                                            08-FEB-2001
                                                                                                                                                                                AAB41790
                                                                                                                                                                                                                AAB41790 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gastrointestinal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAY-2000;
               immunostimulant; thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ABB89040-ABB90444) useful
                                                                                                                                                                                                                                                                                                         326
                                                                                                                                                                                                                                                                                                                                             165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155
                                                                                                                                                                                                                                                                                                                                                                                                                 114 DSAFIVRLETMFAKVIVRPDKVLNYENRSFPLLESEHCGTAGY-----IISREAMR 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 TLTKGEVGCFLSHYSIWEEVVARGLARVLVFEDDVRFESNFRGRLERLMEDV-EAEKLSW 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 VISLASAAERRAHIADTFGSRGIPFQFFDA----LMPSERLEQAMAELVPGLSAHPY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      parasitic infections.

e: The sequence data for this patent did not form part of the nted specification, but was obtained in electronic format directions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LSGVEKACFMSHAVLWEQALDEGLPYIAVFEDDVLLG---EGAEQFLAEDTWLEERFDK 113
                                                                                                                                                                                                                                                                                                         RMLPVDEFLPIMFDQHPNEQYKA-----HFWPRD-LVAFSAQPLLAA-PTHYA 371
                                                                                                                                                                                                                                                                                                                                         FFL--DRFAVL-----PPERIKAVDLMMFTYFFDKEGMPVYQVSPALCTQELHYA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VISLARRPDRRERMLASIWEMEISGRVVDAVDGWMLNSSAIRNLGVDLLPGYQ-DPYSGR 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL89862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-205515P.
                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID NO 1829; 2081pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pulmonary, cardiovascular, renal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.0%;
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                                                                                                                                                                                                                                                                                                                                                                             VNPEKETAVEGLPGLVVAGYSYWTLAYALRLAGARKLLASQPLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to novel genes (ABL89449-ABL90853) and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
                                                                                                                                                                                                                  517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 129.5;
Pred. No. 3.
               coagulant; vasotropic;
                                                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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               antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              format directly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crohn's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bone
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DSAFIVRLETMFAKVIVRPDKVLNYENRSFPLLESEHCGTAGY----

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                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hyperthematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; noottopic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antianaemic; gene therapy; cancer; proliferative disorder; hyperte neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; A
                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                          antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
antidiabetic; hypotensive; dermatological; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 2331-2332; 5507pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-1999;
02-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory; antibacterial; antiviral; antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bone damage; cartilage damage; antiinflammatory disease;
   305
                                                                     246 VISLARRPDRRERMLASLWEMEISGRVVDAVDGWMLNSSAIRNLGVDLLPGYQ-DPYSGR 304
                                       58
                                                                                                                                                                       Local
                                                                                                                 5 VISLASAAERRAHIADTFGSRGIPFQFFDA----LMPSERLEQAMAELVPGLSAHPY--- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-602362/57.
DB; AAC75999.
TLTKGEVGCFLSHYSIWEEVVARGLARVLVFEDDVRFESNFRGRLERLMEDV-EAEKLSW 363
                                     -LSGVEKACFMSHAVLWEQALDEGLPYIAVFEDDVLLG---EGAEQFLAEDTWLEERFDK 113
                                                                                                                                                       59;
                                                                                                                                                                       Similarity
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                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                 AA;
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99US-0127636
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                                                                                                                                                                       9.0%;
                                                                                                                                                       36;
                                                                                                                                                                       Score 129.5;
Pred. No. 4.8
                                                                                                                                                       Mismatches
                                                                                                                                                                       4.8e-05;
                                                                                                                                                                                         DB 21;
                                                                                                                                                     95;
                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antirheumatic;
                                                                                                                                                                                             517;
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                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                    clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUL-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; SEQ ID NO 2591; 1380pp + sequence listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to primers for synthesising full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-2000; 2000EP-0114089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
     114
                                                         305
                                                                                                                                                                       246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      417 RMLPVDEFLPIMFDQHPNEQYKA-----HFWPRD-LVAFSAQPLLAA-PTHYA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364
                                                                                                                58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primers useful for synthesizing full length cDNA clones and their
DSAFIVRLETMFAKVIVRPDKVLNYENRSFPLLESEHCGTAGY------IISREAMR 164
                                                      TLTKGEVGCFLSHYSIWEEVVARGLARVLVFEDDVRFESNFRGRLERLMEDV-EAEKLSW 363
                                                                                                                                                                 VISLARRPDRRERMLASLWEMEISGRVVDAVDGWMLNSSAIRNLGVDLLPGYQ-DPYSGR 304
                                                                                                                                                                                                                     VISLASAAERRAHIADTFGSRGIPFQFFDA----LMPSERLEQAMAELVPGLSAHPY---
                                                                                                          -LSGVEKACFMSHAVLWEQALDEGLPYIAVFEDDVLLG---EGAEQFLAEDTWLEERFDK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FFL - - DRFAVL - -
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59; Conserv
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2000JP-0118774.
2000JP-0183765.
                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            ΑA;
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a T, Nagai
                                                                                                                                                                                                                                                                                                      Score 129.5; DB 2
Pred. No. 4.8e-05;
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K, Kojima
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3, Otsuki
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                                                                                                                                                                                                                                                                              Indels
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T, Koga
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                              molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                             The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA.
                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; SEQ ID NO 2599; 1380pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                   830\ \mbox{Primers} useful for synthesizing full length cDNA clones and use in genetic manipulation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM93206 standard;
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 114
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                                                                                                                                                           Local
                                                                                                               5 VISLASAAERRAHIADTFGSRGIPFQFFDA----LMPSERLEQAMAELVPGLSAHPY---
DSAFIVRLETMFAKVIVRPDKVLNYENRSFPLLESEHCGTAGY ---
                            TLTKGEVGCFLSHYSIWEEVVARGLARVLVFEDDVRFESNFRGRLERLMEDV-EAEKLSW
                                                                                      VISLARRPDRRERMLASLWEMEISGRVVDAVDGWMLNSSAIRNLGVDLLPGYQ-DPYSGR
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                                                      -LSGVEKACFMSHAVLWEQALDEGLPYIAVFEDDVLLG---EGAEQFLAEDTWLEERFDK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-524255/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        full length cDNA; cDNA synthesis; oligo-capping
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su A, Sugiyama
                                                                                                                                                           Similarity
                                                                                                                                                                                                     517 AA;
                                                                                                                                              Conservative
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2000JP-0183765
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25.1%;
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na T, Nagai
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                                                                                                                                              36;
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                                                                                                                                                           Score 129.5; DB 2
Pred. No. 4.8e-05;
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                                                                                                                                              Mismatches
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K, Kojima
                                                                                                                                                                         DB 22;
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                                                                                                                                              Indels
                                                                                                                                                                         Length
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T, Kc
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Qy

165

FFL--DRFAVL-----PPERIKAVDLMMFTYFFDKEGMPVYQVSPALCTQELHYA 212

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Best Local
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.1257
                                                                                                                                                                                                                                                to AAG81453. The secreted proteins can be used for directing the secretion of proteins of interest from a host cell including bacteria, fungal cells, and cultured higher eukaryotic cells. The present invention also describes fusion proteins, where a secreted protein of the invention is operably linked via a peptide bond or peptide linker to a second protein selected from the group consisting of maltose binding protein, an immunoglobulin constant region, a polyhistidine tag and a peptide given in AAG81453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted protein; secretion; bacterial cell; fungal cell; eukaryotic cell; fusion protein; maltose binding protein; immunoglobulin constant region; polyhistidine tag.
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polypeptide for directing secretion of proteins of interest from a host cell including, e.g. bacteria, includes contiguous amino acid residues of polypeptide with specified amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conklin DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ZYMO ) ZYMOGENETICS
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  442
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                                                                                                                                                                                 Local Similarity
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  DLIYLGRKQ----
                                                                                                                                     VISLASAAERRAHIADTFGSRGIPFQFFDA----LMPSERLEQAMAELVPGLSAHPY---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :: | :
DLIYLGRKQ----
                           DSAFIVRLETMFAKVIVRPDKVLNYENRSFPLLESEHCGTAGY-----IISREAMR 164
                                                                                                           VISLARRPDRRERMLASLWEMEISGRVVDAVDGWMLNSSAIRNLGVDLLPGYQ-DPYSGR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEL--DRFAVL-----PPERIKAVDLMMFTYFFDKEGMPVYQVSPALCTQELHYA 212
                                                      TLTKGEVGCFLSHYSIWEEVVARGLARVLVFEDDVRFESNFRGRLERLMEDV-EAEKLSW 441
                                                                      -LSGVEKACFMSHAVLWEQALDEGLPYIAVFEDDVLLG---EGAEQFLAEDTWLEERFDK 113
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                                                                                                                                                                                                                                                                                                                                                                                       Page 121-122; 617pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
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                                                                                                                                                                  Conservative
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-VNPEKETAVEGLPGLVVAGYSYWTLAYALRLAGARKLLASQPLR
                                                                                                                                                                  36;
                                                                                                                                                                              Score 129.5; DB 2
Pred. No. 5.6e-05;
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                                                                                                                                                                  Mismatches
                                                                                                                                                                                            DB 22;
                                                                                                                                                                  95;
                                                                                                                                                                  Indels
                                                                                                                                                                                            Length
                                                                                                                                                                                              578;
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  494
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RESULT 12
AAY30812
ID AAY30
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09-FEB-1998;
09-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secreted protein; prevention; treatment; protein therapy; gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder; blood disorder; developmental abnormality; fetal deficiency; leukemia; autoimmune; acne; hepatic disease; renal disease; lymphoma; inflammation; allergy; asthma; hlzheimer's disease; cognitive disorder; schizophrenia; obesity; sepsis; osteoporosis; arthritis; infection; AIDS; connective tissue disorder; transplant rejection; diabetes; psoriasis; cardiovascular disorder; reproductive disorder; food additive; food preservative; human; primer;
                                                                                                                                                                                             polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for the polynucleotides of the invention based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental treatment of cancer, tumours, neurodegenerative disorders, developmental
                                                                                                                                                                                                                                                                     proteins they encode. The polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polypeptides. Specific meas are Accounted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Куаw Н,
Shi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-FEB-1998;
09-FEB-1998;
                 reproductive disorders. The polypeptides or polynucleotides used as food additives or preservatives. The polypeptide are for identifying their binding partners. This sequence repressecreted protein described in the invention.
                                                                                                                                                                  abnormalities and fetal deficiencies, blood disorders, leukemias, diseases of the immune system, autoimmune diseases, hepatic and r
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1b; Page 206-208; 263pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated human genes potentially useful for, e.g. developmental abnormalities and fetal deficiencies
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                                                                                                                              disorders,
                                                                                                                                              disease, lymphomas, inflammation, allergies, Alzheimer's and cognitive
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                                                                                       ders, schizophrenia, obesity, osteoporosis, arthritis, infections, connective tissue disorders, transplant rejection, diabetes, a, sepsis, acne, pscriasis, cardiovascular disorders, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
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lei Y;
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98US-0074118.
98US-0074141.
98US-0074157.
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                                                                                                                                                                                                                                                                                                                                                                                                                   English.
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RESULT 13
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Best Local
                                                                                                                                                                                                                                                        17-NOV-1998;
22-DEC-1998;
16-MAR-1999;
27-APR-1999;
       Secretory proteins play important roles in the proliferation control, differentiation induction, the material transport and the biophylaxis cells. Membrane proteins have important roles as signal receptors, ion
channels
                                                                                           Proteins comprising hydrophobic regions, such as secretory and membrane proteins, useful in research and diagnostics and having various activities e.g. immunomodulatory, antiinflammatory, chemokinetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                           Claim 1;
                                                                                                                                                                                                         (SAGA
                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB12121 standard;
                                                                                                                                             WPI; 2000-387753/33.
N-PSDB; AAA60183, AAA60193
                                                                                                                                                                                                                                               19-MAY-1999;
                                                                                                                                                                                                                                                                                                                    17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                           25-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; membrane protein; hydrophobic proliferation control; differentiation induction; mater
                                                                                                                                                                                                                                                                                                                                                                                                                            haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                       biophylaxis; signal receptor; ion channel; transporter; immunostimulant;
immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   442
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                                                                                                                                                                                                                                                                                                                                                                                         sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FFL--DRFAVL-----PPERIKAVDLMMFTYFFDKEGMPVYQVSPALCTQELHYA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSAFIVRLETMFAKVIVRPDKVLNYENRSFPLLESEHCGTAGY-----IISREAMR 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VISLARRPDRRERMLASLWEMEISGRVVDAVDGWMLNSSAIRNLGVDLLPGYQ-DPYSGR
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                                                                                                                                                                                                         SAGAMI CHE
PROTEGENE
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                                                                                   thrombolytic
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                                                                                                                                                                                                                                                                                                                                                                                                                            thrombolytic;
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                                                           184-186;
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99JP-0119299.
99JP-0138169.
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                                                                                                                                                                                                                      RES
                                                                                                                                                                                                                                                                                                                                                                                                               olytic; anti-inflammatory; tumour inhibition Alzheimer's disease; Parkinson's disease;
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25.1%;
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Pred. No. 5.6
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present
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sequence is a human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              material transport;
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protein
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which
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of
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RESULT 14
ABP42016
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                has at least one hydrophobic domain. This protein may be a secretory or a membrane protein. The present protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, haematopoiesis activity, tissue growth activity, haemostatic activity, chemotactic/Chemokinetic activity, haemostatic and thrombolytic activity, anti-inflammatory activity and tumour inhibition activity. The present protein could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's
                                                                                                                                                                                                                                                                                                                                           Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndro PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening;
                                                                                                                                                                                                                                                                                                  antibody preparation;
antiinflammatory; gyna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease,
                                           N-PSDB;
                                                                                                                                               07-JUN-2000; 2000US-209467P
                                                                                                                                                                               07-JUN-2001; 2001WO-US18569
                                                                                                                                                                                                                                                                                                                  gene therapy; chromosome mapping;
antibody preparation; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ovarian antigen HFKHF51,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-AUG-2002
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                                                                                                                                                                                                                                            WO200200677-A1
                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                   (HUMA-) HUMAN GENOME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLTKGEVGCFLSHYSIWEEVVARGLARVLVFEDDVRFESNFRGRLERLMEDV-EAEKLSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -LSGVEKACEMSHAVLWEQALDEGLPYIAVFEDDVLLG---EGAEQFLAEDTWLEERFDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VISLARRPDRRERMLASLWEMEISGRVVDAVDGWMLNSSAIRNLGVDLLPGYQ-DPYSGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VISLASAAERRAHIADTFGSRGIPFQFFDA----LMPSERLEQAMAELVPGLSAHPY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RMLPVDEFLPIMFDQHPNEQYKA-----HFWPRD-LVAFSAQPLLAA-PTHYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59;
                                          ABQ55093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                       Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         595 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                       CA
                                                                                                                                                                                                                                                                                                    gynaecological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.0%;
25.1%;
                                                                                                                     SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              636
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Pred. No. 5.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
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                                                                                                                                                                                                                                                                                                  forensic analysis; immunomodulatory; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO:3148
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                                                                                                                                                                                                                                                                                                                  neuroprotective;
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                                                                                                                                                                                                                                                                                                                                                                                                           syndrome;
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useful in the prevention,

molecules encoding novel ovarian polypeptides, ion, treatment and diagnosis of cancer (e.g.

Isolated nucleic acid

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RESULT 15
AAB41900
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                 Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, pastratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic characters, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABC54131-ABC55305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                         08-FEB-2001
                                                                                                                                                                                                                                                                                    AAB41900 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurological diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 TLTKGEVGCFLSHYSIWEEVVARGLARVLVFEDDVRFESNFRGRLERLMEDV-EAEKLSW 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -LSGVEKACFMSHAVLWEQALDEGLPYIAVFEDDVLLG---EGAEQFLAEDTWLEERFDK 113
                                                                                                                                     ORFX ORF1664 polypeptide sequence SEQ ID NO:3328
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Pred. No. 6.4e-05;
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5 VISLASAAERRAHIADTFGSRGIPFQFFDAL----MPSERLEQAMAELVPGLSAHPY---

Query Match Matches

Local

Similarity

8.8%; 23.8%;

Conservative

45;

Score 127; DB 21; Pred. No. 9e-05; 5; Mismatches 120;

Length 521; Indels

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Sequence

521 AA;

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RFDKDSAFIVRLETMFAKVIVRPDKVLNYENRSFPLLESEHC-GTAGYIISREAMRFFLD 168 PLTKGELGCFLSHYNIWKEVVDRGLQKSLVFEDDLRF----EIFFKRRLMNLMRDV-ERE -LSGVEKACFMSHAVLWEQALDEGLPYIAVFEDDVLLGEGAEQF-----LAEDTWLEE 109

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31-MAR-1999;
02-APR-1999;
05-APR-1999;
30-MAR-2000;
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                                                                                                                                             nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypettension, hypothyroidism, cholesterol ester storage, systemic luph hypettension, hypothyroidism, cholesterol ester storage, systemic luph
                                                                                                                                                                                                                                                                                                                                                                                           AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; noottopic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
                                                           allergies, aplastic anaemia, burns, wounds, bone and cartilage on nocturnal haemoglobinuria, antiinflammatory disease; to enhance
                                                                                                                                                                                                                                                           antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The
                                                                                                                                                                                                                                                                                                                                                  immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
antidiabetic; hypotensive; dermatological; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
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N-PSDB; AAC76109.
                                                                                                       erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 2519-2520; 5507pp; English.
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                                      coagulation;
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Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4049, Ap Patent No. 5210183 Sequence 67, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 3, Appli

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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.
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4: //gn2_6/ptodata/1,
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
TVDE: amino acid
TVDE: amino acid
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GENERAL INFORMATION:
                                                                             Matches
                                                                                                     Query Match
                                                                                                                                                                                                                              NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1684
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/312,387B FILING DATE: July 7, 1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Jackson Esq., David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING
                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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ZIP: 07601
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US-09-057-969-3
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US-08-242-932-2
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US-09-134-001C-4049

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Database :

Post-processing:

Maximum Minimum Total number

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length:

Perfect score:

Scoring table: Sequence Title: OM protein -

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; Sequence 6, Application US/08683426
; Patent No. 5705367
; GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING T
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                    Score 1440;
Pred. No. 7e-
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-683-458-6
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US-08-683-458-6
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,458
                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acid
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APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
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                              121 LETMFAKVIVRPDKVLNYENRSFPLLESEHCGTAGYIISREAMRFFLDRFAVLPPERIKA 180
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095A
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CLASSIFICATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1684
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
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FILING DATE: September 26,
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                          Local Similarity
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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STATE: New Jersey
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STREET: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
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Pred. No. 7e-155;
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Best Local Similarity
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 280 amino acid
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NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 30,
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                               TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
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VDLMMFTYFFDKEGMPVYQVSPALCTQELHYAKFLSQNSMLGSDLEKDREQGRRHRRSLK
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VENTION: METHOD OF TRANSFERRING AT LEAST TWO
VENTION: SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSFERASE,
VENTION: POLYGLYCOSYLTRANSFERASE AND GENE ENCODING A
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Pred. No. 7e-155;
n: Mismatches 0;
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241 VMFDLKRALGKFGREKKKRMERQRQAELEKVYGRRVILFK 280

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SEQUENCE DESCRIPTION: SEQ ID NO: US-09-333-412-6
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US-09-333-412-6
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 6:
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LENGTH: 280 amino acids
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TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/312,387 FILING DATE: July 7, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Klauber & Jackson
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TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
OLIGOSACCHARIDES, AND GENES ENCODING THEM
                                                                                                                  LETMFAKVIVRPDKVLNYENRSFPLLESEHCGTAGYIISREAMRFFLDRFAVLPPERIKA 180
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                                                    VDLMMFTYFFDKEGMPVYQVSPALCTQELHYAKFLSQNSMLGSDLEKDREQGRRHRRSLK
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NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
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CLASSIFICATION: <Unknown>
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Pred. No. 7e-155;
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MOLECULE TYPE: US-09-338-943-6
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NAME: Laura A. Coruzzi

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7188-

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEY: 66141 PENNIE

INFORMATION FOR SEO ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 280 amino acids

TYPE: mino acids
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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STATE: New York
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                                                          VDLMMFTYFFDKEGMPVYQVSPALCTQELHYAKFLSQNSMLGSDLEKDREQGRRHRRSLK
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VENTION: METHOD OF TRANSFERRING AT LEAST TWO
VENTION: SACCHARIDE UNITS WITH A POLYGLYCOSYI
VENTION: POLYGLYCOSYLTRANSFERASE AND GENE ENC
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GENERAL INFORMATION:

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TELEX: 133521
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 amino acids
TYPE: amino acid
TYPE: amino acid
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Sequence 8, Application US/08683426 Patent No. 5705367
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Best Local Similarity
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1684
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
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                                                                                                                  241 PANTFKHR-----
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FILING DATE: July 7, 1994
CLASSIFICATION: 435
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STATE: New Jersey
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RESULT 10
US-08-683-458-8
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Best Local Similarity 71.6%;
Matches 209; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 279 amino acids
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095B
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Klauber & Jackson
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TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
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TELEFAX: 133521
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                                                                           241 PANTFKHR-----LIRALTKIGREREKRRQRR-----EQLIGKIIVPFQ 279
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FILING DATE: September 26, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                                                                ----RHRRSLKVMFDLKRALGKFGREKKKRMERQRQAELEKVYGRRVILFK 280
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SYSTEM: PC-DOS/MS-DOS
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; Pred. No. 3.5e-109;
24; Mismatches 34;
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Sequence 8, Application US/08683458 Patent No. 5798233
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.

TITLE OF INVENTION:

Gotschlich, Emil C

GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS

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US-08-878-360-8
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                                                                                               Sequence 8, Application US/08878360 Patent No. 5945322
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 209;
            GENERAL INFORMATION:
APPLICANT: GOTSCHIICH, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THE
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 133521
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 279 amino acids
CORRESPONDENCE ADDRESS
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,458
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
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CLASSIFICATION: 435
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CITY: Hackensack
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.0%; Score 1036.5; DB 1; 71.6%; Pred. No. 3.5e-109; 71.6%; Mismatches 34;
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                               AND GENES ENCODING THEM
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US-09-333-412-8
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STREET: 41
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; MOLECULE TYPE: protein US-08-878-360-8
                                                                          Sequence 8, Application US/09333412
Patent No. 6342382
GENERAL INFORMATION:
GOTSCHICH, Emil C.
APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPHONE: 201 343-1684
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INFORMATION FOR SEQ ID NO:
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LENGTH: 279 amino acid
TYPE: amino acid
TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PC-DASE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,360
FILING DATE: 18-JUN-1997
CLASSIFICATION: 435
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
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FILING DATE:
APPLICATION NUMBER:
FILING DATE: Septemb
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STATE: New Jersey
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                    CORRESPONDENCE ADDRESS
                                        NUMBER OF SEQUENCES:
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ADDRESSEE: Klauber & Jackson
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411 Hackensack Avenue
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                                                               OLIGOSACCHARIDES,
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Pred. No. 3.5
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                                                               AND
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                                                               GENES ENCODING
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US-08-646-590B-40
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                                                                                                                                                                         Patent No. 5962283
GENERAL INFORMATION:
                                                                                                                                                                                             Sequence 40, Application US/08646590B Patent No. 5962283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 8:
                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C
                                                                                                               APPLICANT: Warren, Patrick V.
APPLICANT: Swanson, Ronald V.
TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 LETMFAKVIVRPDKVLNYENRSFPLLESEHCGTAGYIISREAMRFFLDRFAVLPPERIKA 180
                                                                                                                                                                                                                                                                                                                                                                                                               181 VDLMMFTYFFDKEGMPVYQVSPALCTQELHYAKFLSQNSMLGSDLEKDREQGR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                              241 PANTFKHR------LIRALTKIGREREKRRQRR-----EQLIGKIIVPFQ
                                                                                                                                                                                                                                                                                                                                                    234 ----RHRRSLKVMFDLKRALGKFGREKKKRMERQRQAELEKVYGRRVILFK
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                                   STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: JACKSON ESG., DAVID A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 07601
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MONHVISLASAAERRAHIAATFGSRGIPFOFFDALMPSERLERAMAELVPGLSAHPYLSG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEKACEMSHAVLWEQALDEGVPYIAVEEDDVLLGEGAEQFLAEDTWLQERFDPDSAFVVR 120
La Jolla
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FILING DATE: 15-Jun-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 411 Hackensack Avenue CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/312,387 FILING DATE: July 7, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 279 amino acids
                                     4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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71.6%;
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%; Pred. No. 3.5e-109;
24; Mismatches 34;
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US-09-412-184-40
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                                                                                               Sequence 40, Application US/09412184 Patent No. 6268188 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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            APPLICANT: Warren, Patrick V.
APPLICANT: Swanson, Ronald V.
TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,171
FILING DATE: 09-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/01094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               139
                                                                                                                                                                                                                                            292 FVNEMRNAFERRRDTAVEELSKIPGMDVV
                                                                                                                                                                                                                                                                                                                                                               194 GMPVYQVSPALCTQELHYAKFL-SQNSMLGSDLEKDREQGRRHRRSLKVMFDLKRALGK- 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 21-January-1997 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Windows95 SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 AKAKELRAKGVDVIGFGAGEPDFDTPDFIKEACIRALREGKTKYAPSAGIPELREAIAEK 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LMPSERLEQAMAELVPGLSAHPYLSGVEKACFMSHAVLWEQALDEG-----LPYIAVFE 88
                                                                                                                                                                                                                                                                                  FGREKKKRMERQRQA---ELEKVYGRRVI 277
                                                                                                                                                                                                                                                                                                                          SMTGWRIGYVACPEE--YAKVIASLNSQSVSNVTTFAQYG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ENRSFPLLESEHCGTAG-YIISREAMRFFL--DRFAVLPPERIKAVDLMMFTY--FFDKE 193
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22.8%;
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RESULT 15
US-08-468-576B-17
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; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-412-184-40
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TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
Sequence 17, Application US/08468576B Patent No. 5955345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.9%; Score 99; DB 4; Length 394 Best Local Similarity 22.8%; Pred. No. 0.0084; Matches 75; Conservative 38; Mismatches 126; Indels
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APPLICATION NUMBER: US/08/646,590

FILING DATE: 08-May-1996

APPLICATION NUMBER: 08/599,171

FILING DATE: 09-FEB-1996

PRIOR APPLICATION DATA: PCT/US97/01094

APPLICATION NUMBER: PCT/US97/01094

FILING DATE: 21-January-1997

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Haile, Ph.D., Lisa A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 09010/017001

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/412,184
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                     292 FVNEMRNAFERRRDTAVEELSKIPGMDVV 320
                                                                                                                                                                                                                                      242
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ZIP: 92037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 LMPSERLEQAMAELVPGLSAHPYLSGVEKACFMSHAVLWEQALDEG------LPYIAVFE 88
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                                                                                                                                                                                                                                    SMTGWRIGYVACPEE--YAKVIASLNSQSVSNVTTFAQYG-----ALEALKNPKSKD 291
                                                                                                                                                                                                                                                                                                                                EEEELKKI-AEFCVERGIFIISDECYEYFVYGDAKFVSPASFSDEVKNITFTVNAFSKSY 241
                                                                                                                                                                                                                                                                                                                                                                            ENRSFPLLESEHCGTAG-YIISREAMRFFL--DRFAVLPPERIKAVDLMMFTY--FFDKE 193
                                                                                                                                                                                                                                                                                                                                                                                                                          EQIRFFGGVP-----VEVPLKKEKGFQLSLEDVKEKVTERTKAIVINSPNNPTGAVY 182
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203 ALCTQELHYAKFLSQNSMLGSDLEKDREQGRRHRRSLKVMFDIKRALGKFGRE : : : : : :: : : : : : : :	
QY 146 -LESEHCGTAGYIISREAMREFLDREAVLPPERIKAVDLMMETYFFDKEGMPVYQVSP 202	
Qy 113 KDSAFIVR145 	
Qy 61VEKACFMSHAVLWEQALDEGLPY-IAVFEDDVLLGEGAEQFLAEDTWLEERFD 112	
Qy 5 VISLASAAERRAHIADTFGSRGIPFQFFDALMPSERLEQAMAELVPGLSAHPYLSG 60	
Query Match 5.8%; Score 83; DB 2; Length 712; Best Local Similarity 20.2%; Pred. No. 1.3; Matches 66; Conservative 59; Mismatches 106; Indels 96; Gaps	
;; TOPOLOGY: linear US-08-468-576B-17	
TERISTICS: amino acids	
TELEPAX: (914) 332-1844 ; TELEPAX: (914) 332-1844 ; INFORMATION FOR SEQ ID NO: 17:	
DOCKET NUMBE ATION INFORM	
: REGISTRATION NUMBER: 33.141	
; FILING DATE: 17-FEB-1989 . APPROBREY ASSENT TRESONABLION.	
; FILING DATE: U4-DEC-1989 ; PRIOR APPLICATION DATA: . ADDITICATION WINDERS IIC 07/212 5/3	
; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 07/441,703	
; APPLICATION NUMBER: US 07/715,181 ; FILING DATE: 14-JUN-1991	
; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 07/872,646	
; APPLICATION NUMBER: US 08/239,276 ; FILING DATE: 05-MAY-1994	
A:	
; APPLICATION NUMBER: US/08/468,576B ; FILING DATE: O6-JUN-1995	
IA:	
OPERATING SYSTEM: System 7.5	
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage	
; ZIP: 1051-514	
STATE: New York	
STREET: 660 White Plains Road	
NCE ADDRESS:	
OF INVENTION: C	
CANT: Rabin, Daniel OF THISTON, DANCESANTO TRIES OF THE	
: GENERAL INFORMATION:	

17;

Search completed: December 2, 2002, 12:03:18 Job time : $13.4223~{\rm secs}$

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Title:
Perfect score:
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1007
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1: /cgn2_6/ptcdata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptcdata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptcdata/1/pubpaa/US06_NEW_PUB.pep:*

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5: /cgn2_6/ptcdata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptcdata/1/pubpaa/US07_PUBCOMB.pep:*

7: /cgn2_6/ptcdata/1/pubpaa/US07_PUBCOMB.pep:*

9: /cgn2_6/ptcdata/1/pubpaa/US09_NEW_PUB.pep:*

9: /cgn2_6/ptcdata/1/pubpaa/US09_NEW_PUB.pep:*

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Listing first 45 summaries
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10 US-09-211-691-2

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10 US-09-815-242-5280

10 US-09-815-242-11519

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                US-09-976-059-14
US-09-861-451A-72
US-09-815-242-11489
US-09-745-763-174
                                                                       US-09-864-761-48086

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Sequence 222, App
Sequence 14, Appl
Sequence 72, Appl
Sequence 11489, A
Sequence 174, App
Sequence 1335, Ap
                                                                                    Sequence 4, Appli
Sequence 48086, A
Sequence 1, Appli
Sequence 1, Appli
Sequence 13499, A
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Sequence 8, Appli
Sequence 2, Appli
Sequence 40, Appl
Sequence 5280, Ap
Sequence 12140, A
Sequence 11519, A
Sequence 11310, A
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us-09-916-790-5	US-09-764-367A-4	US-09-815-242-10895	US-09-844-006A-2	US-09-815-242-13684	US-09-817-764-4	US-09-864-761-33635	US-09-801-368-306	US-09-815-242-13689	US-09-925-300-1620	US-09-902-941-1906	US-09-801-368-368	US-09-841-132-592	US-09-903-012-32	US-09-887-586A-32	US-09-737-149-2	US-09-815-242-12656	US-09-815-242-5389	US-09-874-923-96	US-09-991-496-96	US-09-874-923-97	US-09-991-496-97	US-09-815-242-13382	US-09-815-242-12608	US-09-815-242-5371	US-09-815-242-4897
Sequence 5, Appli	Sequence 4, Appli	Sequence 10895, A	Sequence 2, Appli	Sequence 13684, A	Sequence 4, Appli		Sequence 306, App	13689,	Sequence 1620, Ap	•	Sequence 368, App	592,	32,	Sequence 32, Appl	Sequence 2, Appli	Sequence 12656, A	5389	Sequence 96, Appl	96, A	Sequence 97, Appl	Sequence 97, Appl	Sequence 13382, A		Sequence 5371, Ap	Sequence 4897, Ap

ALIGNMENTS

US-10-007-267-6
; Sequence 6, Application US/10007267
; Patent No. US20020127682A1
; GENERAL INFORMATION: RESULT 1 TELEX: 133521
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS: COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA: TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800 TELEFAX: 201 343-1684 PRIOR APPLICATION DATA: CORRESPONDENCE ADDRESS: APPLICANT: GOTSCHIICH, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
OLIGOSACCHARIDES, AND GENES ENCODING THEM ATTORNEY/AGENT INFORMATION: NUMBER OF SEQUENCES: APPLICATION NUMBER: US/10/007,267 FILING DATE: 03-Dec-2001 CLASSIFICATION: <Unknown> APPLICATION NUMBER: US/09/333,412 FILING DATE: 15-Uun-1999 APPLICATION NUMBER: 08/312,387 FILING DATE: July 7, 1994 NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1-095 COUNTRY: USA STATE: New Jersey CITY: Hackensack STREET: 411 Hackensack Avenue ADDRESSEE: Klauber & Jackson LENGTH: 280 amino acids 0760 Version #1.25

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Patent No. US20020127682A1
GENERAL INFORMATION:
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                                 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
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FILING DATE: 03-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Jun-1999
APPLICATION NUMBER: 08/312,387
FILING DATE: July 7, 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MQNHVISLASAAERRAHIADTFGSRGIPFQFFDALMPSERLEQAMAELVPGLSAHPYLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: GLYCOSYLTRANSFERASES
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TYPE: amino acid
                                                                                       TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New Jersey
               LENGTH: 279 amino acids
                                                                       TELEX: 133521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 411 Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Klauber & Jackson
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Pred. No. 2.3e-138;
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                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Neisseria meningitidis US-09-211-691-2
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; LENGTH: 275
; TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09211691 Patent No. US20020034805A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 72.0%; Score 1036.5; DB Best Local Similarity 71.6%; Pred. No. 1.6e-97; Matches 209; Conservative 24; Mismatches 34
                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gilbert, Michel
APPLICANT: Young, N. Martin
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wational Research Council of Canada
TITLE OF INVENTION: Fusion Proteins for Use in
TITLE OF INVENTION: Oligosaccharides
FILE REFERENCE: 019957-012910US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: US 60/069,443
PRIOR FILING DATE: 1997-12-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1
NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin V
 181
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                                                                                                                                                                                                                                 1 MQNHVISLASAAERRAHIADTFGSRGIPFQFFDALMPSERLEQAMAELVPGLSAHPYLSG
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                  VDLMMFTYFFDKEGMPVYQVSPALCTQELHYAKFLSQNSMLGSDLEKD----REQGRRHR
                                                                                                      LETMFAKVIVRPDKVLNYENRSFPLLESEHCGTAGYIISREAMRFFLDRFAVLPPERIKA 180
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                                                                                                                                         VEKACFMSHAVLWKQALDEGLPYITVFEDDVLLGEGEEKFLAEDAWLQERFDPDTAFIVR
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                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                   69.9%; Score 1007; DB 1074.7%; Pred. No. 1.5e-94.74.1ve 20; Mismatches 4.
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Best Local Similarity
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    RESULT 5
US-09-815-242-5280
S-09-815-242-5280
Sequence 5280, Application
Patent No. US20020061569A1
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US-09-905-173-40
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LENGTH: 394
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CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: US 09/412,184
PRIOR FILING DATE: 1999-10-04
PRIOR APPLICATION NUMBER: US 09/389,537
PRIOR APPLICATION NUMBER: US 09/389,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1996-05-08
PRIOR APPLICATION NUMBER: US 08/599,171
PRIOR FILING DATE: 1996-02-09
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APPLICANT: SWANSON, Ronald V.
APPLICANT: MATHUR, EIC J.
TITLE OF INVENTION: ENZYMES HAVING TRANSAMINASE AND AMINOTRANSFERASE ACTIVITY AND METTITLE OF INVENTION: USE THEREOF
FILE REFERENCE: DIVER1240-7
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PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: US 09/069,226
PRIOR FILING DATE: 1998-04-27
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PRIOR APPLICATION NUMBER:
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                                                                                                                                                                   FGREKKKRMERQRQA---ELEKVYGRRVI 277
                                                                                                                                                                                                         SMTGWRIGYVACPEE--YAKVIASLNSQSVSNVTTFAQYG---
                                                                                                                                                                                                                                                                                                                              ENRSFPLLESEHCGTAG-YIISREAMRFFL--DRFAVLPPERIKAVDLMMFTY--FFDKE 193
                                                                                                                                                                                                                                                                                                                                                                      EQIRFFGGVP------VEVPLKKEKGFQLSLEDVKEKVTERTKAIVINSPNNPTGAVY 182
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22.8%;
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                         US/09815242
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
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SOFTWARE: FastSEQ for
SEQ ID NO 5280
LENGTH: 657
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Best Local (
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                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                 APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W
APPLICANT: Xu, H. Howard TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes
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PRIOR APPLICATION NUMBER: 60/269,308
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PRIOR APPLICATION NUMBER: 60/257,931
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les 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                            SFPLLESEHCGTAGYIISREAMRFFLDRFAVLPPERIKAVDLMMFTYFFDKEGM 195
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Zyskind, Judith W.
                                                                                   Carr, Grant J.
Yamamoto, Robert T.
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                                                                                                                           Trawick, John D.
                                                                                                                                            Wall, Daniel
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                                                                                                                                                                                                                                                                    Application US/09815242
                                                                                                                                                                   Judith W.
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                                              of Essential Genes
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Length 657; Indels

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                                                                                                                                                                 FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                         PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                    APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Haselbeck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              614 ASPLGWHKYVGTAGKVIA-----IDGFGASAPG-----DLVVEKYGFTKENI 655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               494 DGNETRVAWEVALESESTPTSLVLTRQNLPVLDVPEDVVEEGVRKGAYTVYGSEETPEFL 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                434 FVFSDYLKPALRLSSIMGLNATFIFTHDSIAVGEDGPTHEPIEQLAGLRAIPNMNVIRPA 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 CFMSHAVLWEQALD------EGLPYIAVFEDDV-----
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                                                                                 APPLICATION NUMBER: 60/
FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/253,625
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FILING DATE: 2000-03-21
                                   APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
FILING DATE:
                        APPLICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFPLLESEHCGTAGYIISREAMRFFLDRFAVLPPERIKAVDLMMFTYFFDKEGM 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLGEGAEQFLAEDTWLEERFDKDSAFIVRLETMFA-----KVIVRPDKVLNYE--NR 141
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Zyskind, Judith W.
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                                                                                                                                                                                                                                                                                                                                             Yamamoto, Robert T.
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23.1%;
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                                                                                                     60/207,727
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US-09-815-242-11519
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Best Local :
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LENGTH: 762
                                                                    SEQ ID NO 11310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11310, Application US/09815242 Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
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PRIOR FILING DATE: 2000-12-2
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                      NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23 PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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                                                                                                                                    PRIOR FILING DATE: 2001-02-16
                                                                                                                                                      PRIOR FILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/257,931
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ORGANISM: Helicobacter pylori
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                                             LENGTH: 856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 460 VELLAALYDEEKERPTYTFLKGVIGKSYAFETALRYGVPPFLI---EKAKAF-----YG 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zyskind, Judith W. Wall, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carr, Grant J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trawick, John D.
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25.0%;
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Pred. No.
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RESULT 10
US-09-864-761-48086
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SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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TITLE OF INVENTION: 13245, A No. US20020160483A1el Human Myotonic Dystrophy Type Prot
TITLE OF INVENTION: Kinase and Uses Therefor
FILE REFERENCE: 10147-57U1
CURRENT APPLICATION NUMBER: US/10/017,216
CURRENT FILING DATE: 2001-10-23
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PRIOR FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2055
TYPE: PRT
ORGANISM: Mus musculus
                                                                   521
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                                                                                                                                                                         187
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                                                                                                                                      461 QDKCHKMEQEMTRLHRRVSEVEAVLSQKEVELKASETQRSLLEQDLATYITECSSLKRSL 520
                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 5.5%;
Local Similarity 17.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 ERLEQAMAELVPGLSAHPYLSGVEKACFMSHAVLWEQALDEGLPYIAVFEDDVLLGE--- 95
                                                                                                                                                                                                                                                                                                             76 ALDEGLPYIAVFEDDVLLGEGAEQFLAEDTWLEERFDKDSAFIVRLETMFAKVIVRPDKV 135
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                                                                   EQARMEVSQEDDKALQLLHDIREQ----SRKLQEIKEQEYQAQVEEM
                                                                                                                                                                       ---TYFFDKE----GMPVYQVSPALCTQELHYAKFLSQNSMLGSD------LEKDR 229
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                                                                                                  EQGR-----RHRRSLKVMFDLKRALGKFGREKKKRMERQRQAELEKV
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21.7%;
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Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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; OTHER INFORMATION: E COTHER INFORMATION: E COTHER INFORMATION: S COTHER INFORMATION: E COTHER INFORMATION: US-09-864-761-48086
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SEQ ID NO 48086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00668
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PRIOR APPLICATION NUMBER: PCT/US01/00665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/608,408 PRIOR FILING DATE: 2000-06-30 PRIOR APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: US 60/234,687
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PRIOR APPLICATION NUMBER: PCT/US01/00663
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PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 222
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IISREAMRFFLDRF 170
                                                  EHYLEDADWFLKADDDTYVILDNLRWLLSK--YDPEEPIYFGRRFKPYVKQGYMSGGAGY 139
                                                                                                    EQFLAEDTWLEERFDKDSAFIVRLETMFAKVIVRPDKVLNYENRSFPLLESEH-CGTAGY 156
                                                                                                                                                                           Similarity
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EXPRESSED IN PLACENTA, SIGNAL = 1.5
SWISSPROT HIT? 050950, EVALUE 4.90e-01
EST_HUMAN HIT: BE336820.1, EVALUE 1.00e-112
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25.7%;
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Pred. No. 1.
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                  US-09-815-242-13499
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US-09-849-562A-1
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                                    RESULT 13
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Patent No. US20020056033A1
GENERAL INFORMATION:
APPLICANT: Cummings, Richard D.
APPLICANT: McEver, Rodger P.
TITLE OF INVENTION: synthetic glycosulfopeptides
FILE REFERENCE: 5820.593
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 363
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Best Local Similarity 25.7%; Pr
10. Conservative 19;
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Sequence 13499, Application US/09815242
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                           Matches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cummings, Richard D.
APPLICANT: McEver, Rodger P.
TITLE OF INVENTION: synthetic glycosulfopeptides and methods of synthesis thereof
FILE REFERENCE: 5820.594
CURRENT APPLICATION NUMBER: US/09/849,562A
CURRENT FILING DATE: 2001-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/849,031A CURRENT FILING DATE: 2001-05-04 PRIOR APPLICATION NUMBER: 09/334,013 PRIOR FILING DATE: 199-06-15 NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 09/334,013
PRIOR FILING DATE: 1999-06-15
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                                                                                            214 VLSKEALKRFVDAF 227
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                                                                                                                                                                   EHYLEDADWFLKADDDTYVILDNLRWLLSK--YDPEEPIYFGRRFKPYVKQGYMSGGAGY 213
                                                                                                                                                                                                   EQFLAEDTWLEERFDKDSAFIVRLETMFAKVIVRPDKVLNYENRSFPLLESEH-CGTAGY 156
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25.78;
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Pred. No. 2
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Pred. No. 2.8;
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APPLICANT:
                  APPLICANT:
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US-09-815-242-13499
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PRIOR FILING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-2
PRIOR FILING DATE: 2000-12-2
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                      Sequence 222, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
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LENGTH: 623
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                                                                                                                     APPLICANT:
                                                                      APPLICANT:
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TITLE OF INVENTION: Identification
TITLE OF INVENTION: Prokaryotes
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                     APPLICANT:
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SOFTWARE: FastSEQ for Windows Version
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                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 PERIKAVDLMMFTYFFDKEGMPVYQVSPALCTQELHYAKFLSQNSM---LGSDLEKDREQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                   544 -----KVVKV------REDKKRMTYQEKQEWASIEG 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 GRRHRRSLKVMFDLKRALGKFGREKKKRMERQRQAELEKVYG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          446 RLYLLKLLLEKPNVLLLDEPTNDLDIATLTVLENFLQGFAGPVLTVSHDRYFLDKVAT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         389 EGLDESKRVINYLQEVAEEVKTSGGSTTSIAE---LLEQFLFPRSTHGTLIEKLSGGEKK 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 QALDEG---LPYIAVFEDDVLLGEGAEQFLAEDTWLEERF------DKD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 5.4%;
Local Similarity 19.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAFIVRLETMFAKVIVRPDKVLNYENRSFPLLESEHCGTAGYIISREAMRFFLDRFAVLP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
                                                                                                                Hecht, Peter
Holtzman, Doug
Madden, Kevin
                                          Maxon, Mary
Milne, Todd
Mo. US20020128250Alman, Thea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamamoto, Robert T.
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Trawick, John D.
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Salama, Sofie
                      Royer, John
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TYPE: PRT
; ORGANISM: Actinoplanes sp.
US-09-976-059-14
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                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.0 SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/09976059 Patent No. US20020164747A1
                                                                                                                                                               Matches
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APPLICANT: Farnet, Chris
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
EILE REFERENCE: 109272.147
CURRENT FILLING DATE: 2001-03-07
CURRENT FILLING DATE: 2001-03-07
CURRENT FILLING DATE: 2001-03-07
                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/976,059
CURRENT FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zazopoulos, Emmanuel
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
FILE REFERENCE: 3019-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR TLING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
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TYPE: PRT
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2950 EVYVAGRO----LARAYLGRAALTGTRFVACPFLPAGERMYRTGDRARWSRGRLQFAGRT 3005
                                                                           2896 LVNMYGITETTVHVTHQDLAPADTTGSPIGRGIPG-----LSVYVLDEALRPVPPGVAG 2949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 TMFAKVIVRPDKVLNYENRSFPLLESEHCGTAGYIIS--REAMRFFLDRFAVLPPERIKA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 VDLMMFTYFFDKEGMPVYQVSPALCTQE-LHYAKFLSQNSMLGS-DLEKDR 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            479 YFSSPFGQQVLSSTFLD----HKLE---
                                    55 HPYLSGVEKACFMSHAVLWEQALD----EGLPYIAVFE-----DDVLLGEGAEQFLAE- 103
                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 HIADTFGSRGIPFQFFDALMPSERLEQAMAELVPGLSAHPYLSGVEK----ACFMSHAVL 72
                                                                                                     5 VISLASAAERRAHI------ADTFGS---RGIPFQFFDALMPSERLEQAMAELVPGLSA 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W-----EQALDEGLPYIAVFEDDVLLGEGAEQFLAEDTWLEERFDKDSAFIVRLE 122
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Similarity 21.8%;
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Silva, Jeff
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Pred. No. 15;
47; Mismatches
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Pred. No. 96;
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Search completed: December 2, 2002, 12:16:05 Job time: 8.61203 secs

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Maximum
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RiTettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Science 287, 1809-1815, 2000
A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; A; Title: Complete genome sequence of Neisseria meningitidis serogroup B A; Reference number: A81000; MUID: 20175755; PMID: 10710307
A; Accession: A81027

C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision
C;Accession: A81027

lacto-N-neotetraose biosynthesis glycosyl transferase LgtE NMB1926 [imported] -

31-Mar-2000 #text_change 19-Jan-2001

Dougherty, Pizza, M.

Rappuoli, R strain MC58 ×.Ε.;

Neiss

A; Status: preliminary

Qy В DЬ Qy DЪ Qy DЪ Qy A;Gene: NMB1926 C;Superfamily: lipopolysaccharide biosynthesis-associated protein A; Cross-references: GB:AE002541; A; Experimental source: serogroup A; Molecule type: DNA A; Residues: 1-280 <TET> Best Loc Matches Query Match 181 181 121 121 61 61 Local 1 MQNHVISLASAAERRAHIADTFGSRGIPFQFFDALMPSERLEQAMAELVPGLSAHPYLSG 60 VMFDLKRALGKFGREKKKRMERQRQAELEKVYGRRVILFK VDLMMFTYFFDKEGMPVYQVSPALCTQELHYAKFLSQNSMLGSDLEKDREQGRRHRRSLK 240 LETMFAKVIVRPDKVLNYENRSFPLLESEHCGTAGYIISREAMRFFLDRFAVLPPERIKA 180 VEKACEMSHAVLWEQALDEGLPYIAVFEDDVLLGEGAEQFLAEDTWLEERFDKDSAFIVR 120 VDWMMFTYFFDKEGMPVYQVNPALCTQELHYAKFLSKNSMLGSDLEKDREQERRHRRSLK VMFDLKRALGKFGREKKKRMERQRQAELEKAYGRRVISFK 11 Similarity 253; Conserv Conservative 89.2%; Score 1284; D Pred. No. 3.3e 9; Mismatches 9 GB:AE002098; NID:g7227175; PIDN:AAF42255.1; PID:g722 B, strain MC58 3.3e-104; DB 2; Length 280; Indels 0; Gaps 240 0;

S70815
glycosyl transferase E (EC 2.4.-.
C;Species: Neisseria meningitidis

<u>.</u>

Neisseria meningitidis

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C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 20-Sep-1999 C;Accession: $70815
R;Jennings, M.P.; Hood, D.W.; Peak, I.R.A.; Virji, M.; Moxon, E.R.
Mol. Microbiol. 18, 729-740, 1995
A;Title: Molecular analysis of a locus for the biosynthesis and phase-variable & A;Reference number: $70812; MUID:96414473; PMID:8817494
A;Accession: $70815
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-276 < ZEN>
A;Cross-references: EMBL:U25839; NID:9973183; PIDN:AAC44086.1; PID:9973187
C;Genetics:
A;Gene: lgtE
C;Superfamily: lipopolysaccharide biosynthesis-associated protein
C;Reywords: glycosyltransferase
                                                                                                                                                                                                                           C;Genetics:
A;Gene: .NMB1928
C;Superfamily: 1
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: C81027
C;Accession: C81027
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.;
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Doughe
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza,
Science 287, 1809-1815, 2000
S;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuc
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B Strain
A;Reference number: A81000; MUID: 20175755; PMID: 10710307
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A; Accession: C81027
A; Status: preliminary
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A; Residues: 1-275 <TET>
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87.9%;
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Pred. No. 4.9e-100;
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                           glycosyl transferase B (EC 2.4...) - Neisseria meningitidis C;Species: Neisseria meningitidis C;Species: Neisseria meningitidis C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 20-Sep-1999 C;Accession: S70814 R;Jennings, M.P.; Hood, D.W.; Peak, I.R.A.; Virji, M.; Moxon, E.R. Mol. Microbiol. 18, 729-740, 1995 Mol. Microbiol. 18, 729-740, 1995 A;Title: Molecular analysis of a locus for the biosynthesis and phase-variable expres A;Reference number: S70812; MUID:96414473; PMID:8817494 A;Accession: S70814
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A;Molecule type: DNA
A;Residues: 1-268 <PAR>
A;Cross-references: GB:AL162753;
A;Cross-references: serogroup
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C;Superfamily:
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C;Genetics:
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04; Conservative
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A;Title: Complete DNA sequence of a serogroup A strain of A;Reference number: A81775; MUID:20222556; PMID:10761919 A;Accession: B81971
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                                                                                                                                                  VDLMMFTYFFDKEGMPVYQVSPALCTQELHYAKFLSQNSMLGSDLEKDREQGRRHRRSLK 240
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24; Mismatches
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A81971
Lacto-N-neotetraose biosynthesis glycosyl transferase NMA0525 [imported] - C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: A81971

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C;Superfamily: lipopolysaccharic
C;Keywords: glycosyltransferase
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C; Superfamily:
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A; Residues: 1-279 < PAR>
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70.4%;
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Pred. No. 5.3e-77;
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Pred. No. 4.2e-80;
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Mungall, K.; Quail, M.A.;
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-EQGRRHR 236
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A; Molecule type: DNA
A; Residues: 1-302 <TIGR>
                                        A; Status: nucleic acid sequence
                                                       A; Reference number: A64000; A; Accession: A64077
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C; Superfamily:
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A; Residues: 1-266 <HIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TMFAKVIVRPDKVLNYENRSFPLLESEHCGTAGYIISREAMRFFLDRFAVLPPERIKAVD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KACFMSHAVLWEQALDEGLPYIAVFEDDVLLGEGAEQFLAEDTWLEERFDKDSAFIVRLE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLMFNIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMMFTYFFDKEGMPVYQVSPALCTQELHYAKFLSQNSMLGSDLEKDREQ--GRRHRRSLK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TFLNFSKCKDKKIKPYSGRKILKLVSENCGAAGYVISREAVKQLSAHICSLTSNHLLAID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PANTFKHRLIRALTKISREREKRRQRR-----EQLIGKIIVPFQ 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NYVISLTSAYQRREHIQKEFSQQNIPFEFFDALKPSKELTSLIEKFIPNL-LHAKLTEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSLKVMFDLKRALGKFGREKKKRMERQRQAELEKVYGRRVILFK 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDWMMFGNPDDRERMPVCQLNPALCAQELHYAKFHDQNSALGSLIEHDRCLNSKQQRRDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lipopolysaccharide biosynthesis-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   required for the biosynthesis of a phase-variable lipopolysaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  -ISLAGKPKK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -NOSTYQVSPGVCVQE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                  ·----ILRKIY-RKLFISK
                                          not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 500.5; DB 2
Pred. No. 4.9e-36;
                                          shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GQLYPKDIKLHSQLETERQKYLSVKKKRTLK
                                          translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN:CAA90892.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98;
                                                                                                                                                                                                                                                                                                                                                                                                260
                                                                                                                                                                                                                                                                                                                                                                                                                                       280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #text_change
                                          not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                          shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lic2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PID:g1150403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-Jun-2000
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                                                                                                                                                               ; Kerlavage
M.; Weidman
gen, N.S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                       Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RM7004
                                                                                                                          Vente
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for
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R; Cope, L.D.;

Yogev, R.;

strain Rd KW20 Mertsola,

J.;

Latimer, J.L.;

Hanson,

M.S.; McCracken Jr.,

G

NID:g1573519; PIDN:AAC22208.1; PID:g1573535

A; Experimental source:

A; Cross-references: GB:U32736; GB:L42023;

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Mol. Microbiol. 5, 1113-1124, 1991
A;Title: Molecular cloning of a gene involved in lipooligosaccharide biosynthesis and v A;Title: Molecular cloning of a gene involved in lipooligosaccharide biosynthesis and v A;Reference number: S15282
A;Accession: S15282
A;Accession: S15282
A;Molecule type: DNA
A;Residues: 1-28,'N',30-40,45-105,'L',107-150,'R',152-302 <COP>
A;Cross-references: EMBL:X56903; NID:948811; PJDN:CAA40221.1; PJD:948812
A;Note: it is uncertain whether Met-1 or Met-11 is the initiator
R;High, N.J.; Deadman, M.E.; Moxon, E.R.
Mol. Microbiol. 9, 1275-1282, 1993
A;Title: The role of a repetitive DNA motif (5'-CAAT-3') in the variable expression of A;Reference number: S39576; MUID:95020659; PMID:7523834
A;Residues: 1-28,'N',30-40,49-105,'L',107-150,'R',152-255,'P',257-273,'D',275-302 <HIG>A;Rosidues: 1-28,'N',30-40,49-105,'L',107-150,'R',152-255,'P',257-273,'D',275-302 <HIG>A;Experimental source: Strain RM7004
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Description: involved in lipooligosaccharide biosynthesis and virulence expression C;Superfamily: lipopolysaccharide biosynthesis-associated protein
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae FA;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: F64091
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-282 <TIGR>
A;Cross-references: GB:U32760; GB:L42023; NID:g1573764; PIDN:AAC22423.1; PID:g15
C;Genetics:
A;Start codon: GTG
                                                                                                                                                                                                                      lipopolysaccharide biosynthesis protein lic2B homolog - Haemophilus influenzae C;Species: Haemophilus influenzae C;Species: Haemophilus influenzae C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 20-Sep-1999 C;Accession: F64091 R;Felsischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Ker Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; W D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, Science 269, 496-512, 1995
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
F64091
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSMLGSDLEKDREQGRRHR-----RSLKVMFDLKRALGKFGREKKKRMERQRQAELEK 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VFLNQNEWLKTRFDFNDIFIIRLETFLQPVKLEKQTKIPPFNSRNFDILKSTHWGTAGYI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MQNHVISLASAAERRAHIADTFGSRGIPFQFFDAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYGRRVILF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSVLTSGLEKERQKRSKIRKKKTLKQRLTRIKENIIRAL----NRKKWKEQQRIKEMQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISQGAAKYVIEYLKNIPSDEIVAVDELIFNKLVDVDNYIVYQLNPAICIQELQANQ---S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISREAMRFFLDRFAVLPPERIKAVDLMMFTYFFDKEGMPVYQVSPALCTQELHYAKFLSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QFLAEDTWLEERFDKDSAFIVRLETMFAKV-IVRPDKVLNYENRSFPLLESEHCGTAGYI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NQSINQSNSILHNIEESRILTKGEKGCLISHFLLWNKCVNENFEYLKIFEDDVILGENAE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQAMAE----LVPGLSAHPYLSGVEKACFMSHAVLWEQALDEGLPYIAVFEDDVLLGEGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IENIVISMENATERRKHITKQFESKKLSFSFFNAYTYQSINQSINQSINQSINQSINQSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           involved in lipooligosaccharide biosynthesis and virulence expression lipopolysaccharide biosynthesis-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                             GB:U32760; GB:L42023; NID:g1573764; PIDN:AAC22423.1; PID:g1573773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.5%;
33.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 438.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.4e-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----MPSERL 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302;
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                                                                                                                                                                                                                                                                                           Kerlavage
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                                                                                                                                                                                  Rd
                                                                                                                                                                                                                                                  N.S.M.
                                                                                                                                                                                                                                                                                                                                                                                  (strain
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                                                                                                                                                                                                                           Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
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A; Map position: I
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Matches
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lipooligosaccharide k
C;Species: Brucella m
C;Date: 01-Feb-2002 #
C;Accession: AD3304
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A;Title: The genome sequence of the facultative intracellular pathogen Brucell A;Reference number: AD3252; PMID:11756888
A;Accession: AD3304
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A; Residues: 1-268 < KUR>
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R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, Nature 397, 176-180, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
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                  뮍
                                            QΥ
                                                                                                                                                                            A; Experimental source: strain
                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-332 <A
                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                            A; Reference number: A71800; A; Accession: E71916
                                                                                                                                                                                                                                                                        A; Title: Genomic sequence comparison of two unrelated isolates of the human A; Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                           C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change
C;Accession: E71916
                                                                                                                                                                                                                                                                                                                                                                                         A; Variety: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                         probable lipopolysaccharide biosynthesis protein -
C;Species: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: AB011156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-738 <NAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; DNA Res. 5, 31-39, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: T00343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein KIAA0584 - human (fragment)
                                                                                                                                                                                            ;Residues: 1-332 <ARN>;Cross-references: GB:AE001489; GB:AE001439;
                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
                                                                                                                                                               Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 A-VLPPERIKAV-----DLMMFTYFFDKEGMPVYQVSPALCTQELHYA---KFLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      458 MINLKRRKDRRDRMLRTLYEQEIEVKIVEAVDGKALNTSQLKALNIEMLPGYRDPYSSRP 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 YLSGVEKACFMSHAVLWEQALDEGLPYIAVFEDDVLLGEGAEQFLAE--DTWLEERFDKD 114
                                                                                              Local
                  G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 VISLASAAERRAHIADTFGSRGIPFQFFDAL----MPSERLEQAMAELVPG----LSAHP 56
                                               4 HVISLASAAERRAHIADT---
                                                                                                                                              jhp0562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIAA0584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTRG-EIGCFLSHYSVWKEVIDRELEKTLVIEDDVRFEHQFKKKLMKLMDNIDQAQLDWE 576
               YIISLKESQRR----LDTEKLVLESNEKFKGRCV-FQIFDAISPKHQDFEKLLQELYNAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIWDNETVATDWDRTHAWKSRKQSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---QNSMLGSDLE-----KDREQGR 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKMLPVDEFLPVMYNKHPVAEYKEYYESRDLKAFSAEP-LLIYPTHYTGQPGYLSDTETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIYIGRKRMQ----VKEPEKAVPNVAN----LVEADYSYWTLGYVISLEGAQKLVGANPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAFIVRLETMFAKVIVRPDK-VLNYENRSFPLLESEHC-GTAGYIISREAMRFFL--DRF 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61;
                                                                                                Similarity
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                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.4%;
                                                                                              8.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coding sequences of unidentified; MUID:98290545; PMID:9628581
                                                                                                                                                                              J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51;
                                                                               47;
                                                                            Score 120.5; DB 2;
Pred. No. 0.0078;
7; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 121; DB 2; Pred. No. 0.019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NID: g3043691; PIDN: BAA25510.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                            FGSRGIPFQFFDALMPSER-LEQAMAELVPGL 52
                                                                                                                                                                                            NID:g4155102;
                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107;
                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 738
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                                                                                                          Length
                                                                                                                                                                                            PIDN:AAD06135.1; PID:g415510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human genes. IX. The complet
                                                                             125;
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                                                                                                                                                                                                                                                                                                                                                                          08-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PID:g3043692
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216
                                                                             21;
                                                                                                                                                                                                                                                                                         gastric path
                                                                                                                                                                                                                                                                                                                                          Smith,
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                                                                                                                                                                                                                                                                                                                                                                                                                           J99)
                                                                                                                                                                                                                                                                                                                         G.F.;
                                                                                                                                                                                                                                                                                                                                          D.R.
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226
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A;Molecule type: DNA
A;Residues: 11-26,'K',28-39,'T',41-55,'S',57-111,'L',113-136,'N',138-139,'N',141-143,
A;Cross-references: EMBL:M94855; NID:g148931; PIDN:AAA24981.1; PID:g148935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;McLaughlin, R.; Abu Kwalk, Y.; Young, R.; Spinola, S.; submitted to the EMBL Data Library, June 1992
A;Description: Characterization and sequence of the lsg l
A;Reference number: S27577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, A;Title: Whole-genome random sequencing and assembly of Haemc A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: E64175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Ko; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision
C;Accession: E64175; S27580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S27580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:L42023; TIGR:H11697
A;Experimental source: strain Rd KW20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-267 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein HI1697 (1sg locus) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 22.1 nes 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MQNHVISLASAAERRAHIADTFGSR--GIPFQFFDALMPSERLEQAMAEL--VPGLSAHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LDSTIQKPQKKSLKSYPLPPQKSTFKNLFYYSLNAKKRLNAFQQYSKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLGSDLEKDREQGRR----
IENPVLISNLESVRGSLSNNLLKKLMKYPLKKIFAIKKNL
                                                  SQNSMLGSDLEKDREQ-----
                                                                                                          YLIKKSAARRFIQQISQNKPFWL-ADDFLLFEQNFNIRNKVVRPL
                                                                                                                                                                                                                  KLEAEIILLGQSKINDFNDFDLEINYPTTFSFLCKKTGDV----NYAFP-YKSYFAGTVG
                                                                                                                                                                                                                                                                       RFDKDSAFI.
                                                                                                                                                                                                                                                                                                                         YFRNVTKGEIGCTLSHLSVYQKIVEDNDIAEDSYALVCEDDALFHSDFQQNLT--ALLSE
                                                                                                                                                                                                                                                                                                                                                                            YLSGVEK---ACFMSHAVLWEQALDEG----LPYIAVFEDDVLLGEGAEQFLAEDTWLEE 109
                                                                                                                                                                                                                                                                                                                                                                                                                              LKKYLISLDKDIQRR----ELFFSQKNTEDFQVFSAINTMQKDWDELAAIFNIEQFKAH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKTFIEATESFKIIEP-----VDMFMDNSAYHDVANLTYVPCPV------SLSEHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FFDVSRFLNLSTHKVIHYILKKIQKSYYATHEKEAFFLEHFYLTSVYVASTAGYYLTPKG
                                                                                                                                                            YIISREAMRFFLDRFAVLPPERIKAVDLMMFTYFFDKEGMPVYQVSPALCTQELHYAKFL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDC-LKSPFD-----FVRLYGCYWYYHETKFHVLPKEFVFPPFDHSFKNN--PILEKFKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDTWLEERFDKDSAFIVRL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SA-----HPY----LSGVEKACFMSHAVLWEQALDEGLPYIAVFEDDVLLGEGAEQFLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.5%;
22.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --HRRSLKVMF----DLKRALGKFGREKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51;
                                                  -GRRHRRSLKVMFDLKRAL
                                                                                                                                                                                                                                                                    -VRLETMFAKVIVRPDKVLNYENRSFPLLESEHCGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 108.5; DE Pred. No. 0.066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --ETMF---AKVIVRPDKVLNYENRSFPLLES---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 110;
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R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKeson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable lipopolysaccharide biosynthesis protein - Helicobacter pylori (strain J99)
c;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb_1999 #sequence_revision 12-Feb-1999 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
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A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: B64623
                                                                                C; Superfamily:
                                                                                                                                                            A;Cross-references: GB:AE001507; GB:AE001439; NID:g4155326; PIDN:AAD06344.1; PID:g41553 A;Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                     A; Title: Genomic sequence comparison of two unrelated isolates A; Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                       R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
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A; Residues: 1-273 < TOM>
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A; Residues: 1-273 < ARN>
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                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                               A; Accession: E71890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lipopolysaccharide biosynthesis-associated protein lex2B - Helicobacter pylori (strain
3;Species: Helicobacter pylori
3;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDITLKEDFKEGL---DFLEKHI-QELGYIRLMHLLYDASVKSEP---LSHKNHEIQERV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QNIKDMGITTNLISEVSKFYYALKYHAKFMSLGELGCYASHYSLWEKCIELN-EAICILE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEQISTIARKEEPYSPKIALMRELHF-KYL 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDVLLGEGAEQFLAEDTWLEERFDKDSAFIVRLETMF-AKVIVRPDKVLNYENRSFP--- 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VCDTF----GLVFRDTTTLLNSINATHHQAQIFDAIY-SKTFEGGLHPLVK-KHLHPYFIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64; Conservative
                                                                              lipopolysaccharide biosynthesis-associated protein
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Score 99; DB 2; Pred. No. 0.45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ACFMSHAVLWEQALDEGLPYIAVFE 88
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                           Length 273;
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they, L.
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                                                                150 YARLMHLLYDASVKSEP-LNHKNQEIQERVGIIKAYSHGVGTQGYVITPKIAKVFLKHSR 208
                                                                                                 118 IVRLETMFAKVIVRPDKVLNYENRSFP-----LLESEHCGTAGYIISREAMRFFL--DR 169
209 KWVVPVDTIMDATFIHGVKNLVLQPFVIADDEQISTIARKEEPYSPKIALMRELHF-KFL
                                 170 FAVLPPERI------KAVDLMMFTYFFDKEGMPVYQ----VSPALC-TQELHYAKFL 215
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                                                                                                                                                                                                           QIFDAIY-SKTFEGGLHPLVK-KHLHPYFITQNIKDMGIATSLISEVSKFYYALKYHAKF 95
                                                                                                                                      MSLGELGCYASHYSLWQKCIELN-EAICILEDDITLKEDFKEGL---DFLEKHIQE--LG 149
                                                                                                                                                                        -----ACFMSHAVLWEQALDEGLPYIAVFEDDVLLGEGAEQFLAEDTWLEERFDKDSAF 117
                                                                                                                                                                                                                                              QFFDALMPSERLEQAMAELVPGLSAHPY - - - -
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                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                               36;
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Search completed: December 2, 2002, 12:00:12 Job time : 14.4266 secs

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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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STRAIN=MC58 / Serogroup B;
MEDLINE-96414473; PubMed-8817494;
MEDLINE-96414473; PubMed I.R.A., Virji M., Moxon E.R.;
Mennings M.P., Hood D., Peak I.R.A., Virji M., Moxon E.R.;
"Molecular analysis of a locus for the biosynthesis and phase-variable expression of the lacto-N-neotetraose terminal lipopolysaccharide expression of the lacto-N-neotetraose structure in Neisseria meningitidis.";
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  Matches
                                                      InterPro; IPR002654; GT_25.

Pfam; PF01755; Glyco_transf_25; 1.

Lipopolysaccharide biosynthesis; Transferase; Gl
SEQUENCE 279 AA; 31776 MW; C2219D1A6119D622
                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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01-NOV-1997 (Rel.
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                               "Genetic locus for the biosynthesis of the variable Neisseria gonorrhoeae lipooligosaccharide."; J. Exp. Med. 180:2181-2190(1994).
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35, Last sequence update)
41, Last annotation update)
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                Score 1036.5;
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16-OCT-2001
Complete
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jennings M.P., Hood D., Peak I.R.A., Virji M., Moxon E.R.; "Molecular analysis of a locus for the biosynthesis and phase-variable expression of the lacto-N-neotetraose terminal lipopolysaccharide structure in Neisseria meningitidis."; Mol. Microbiol. 18:729-740(1995).
                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entitles requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                     Science 287:1809-1815(2000).
-!- FUNCTION: ADDS THE SECOND GALACTOSE TO
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MEDLINE=96414473; PubMed=8817494;
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15-JUN-2002 (Rel. 41, Last annotation update)
Lacto-N-neotetraose biosynthesis glycosyl transferase lgtB
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              InterPro; IPR002654; GT_25.
Pfam; PF01755; Glyco_transf_25; 1.
Pfam; PF01755; Glyco_transf_25; Transferase; Glycosyltransferase;
                                                                                    TIGR; NMB1928;
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MEDLINE=20175755; PubMed
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Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroy
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis 22491.";
Nature 40%.50.
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                           InterPro; IPR002654; GT_25.
Pfam; PF01755; Glyco_transf_25; Lipopolysaccharide biosynthesis;
                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                               use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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MEDLINE=20222556; PubMed=10761919;
 SEQUENCE
                Complete
                                                                     EMBL; AL162753; CAB83817.1; -.
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15-JUN-2002
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    Transferase; Glycosyltransferase;

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                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institute. There are no restrictions modified and this statement is not removed. Usage by and for no entities requires a licence according to the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-RM 7004 / Serotype B;
High N.J., Jennings M.P., Moxon R.E.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: INVOLVED IN EXTRACELLULAR LIPOOLIGOSACCHARIDES
BIOSYNTHESIS AND VIRULENCE EXPRESSION. INVOLVED IN THE SY
OF THE OLIGOSACCHARIDE MOIETY OF THE LOS MOLECULE BY ADDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There \varepsilon
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AC Q03974

DT 01-NOV

DT 01-NOV

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MEDLINE-95350630; PubMed="542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.

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Mol. Microbiol. 9:1275-1282(1993).

-!- FUNCTION: INVOLVED IN EXTRACELLULAR LIPOOLIGOSACCHARIDES (LOS BIOSYNTHESIS AND VIRULENCE EXPRESSION. INVOLVED IN THE SYNTHE OF THE OLIGOSACCHARIDE MOIETY OF THE LOS MOLECULE BY ADDING OF THE OLIGOSACCHARIDE MOIETY OF THE LOS MOLECULE BY ADDING OF THE GLYCOSYLTRANSFERASE FAMILY 25.
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Cope L.D., Yogev R., Mertsola J.,
McCracken G.H. Jr., Hansen E.J.;
                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=RM 7004 / Serotype B;
MEDLINE=95020659; PubMed=7523834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning of a gene involved biosynthesis and virulence expression
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                                                                                                                     CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-11 IS THE INITIATOR.
                             SWISS-PROT entry is copyright. It is produced through a sen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microbiol. 5:1113-1124(1991).
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STRAIN-Serotype A1;
MEDLINE=95301198; PubMed=7781993;
Potter M.D., Lo R.Y.C.;
"Cloning and characterization of a gene from Pasteurella A1 involved in lipopolysaccharide biosynthesis.";
FEMS Microbiol. Lett. 129:75-81(1995).
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                                                                                                                                                                                                                                                             Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e; Glycosyltransferase; V
29 29 K -> V
63 70 MISSI
67 70 MISSI
106 F -> I
151 151 Q -> I
256 256 S -> I
274 274 N -> I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302
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33,
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Last
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                                                                                                                                                                                                                                                             gamma subdivision; Pasteurellaceae;
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K -> N (IN STRAINS DL42 AND RM 7004)

MISSING (IN STRAIN DL42).

MISSING (IN STRAIN DL42).

F -> L (IN STRAINS DL42 AND RM 7004)

C -> R (IN STRAINS DL42 AND RM 7004)

S -> D (IN STRAIN RM 7004).

N -> D (IN STRAIN RM 7004).
                                                                                                                                                                                                                                                                                                                                                                             sequence
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Pred. No. 1.2e
58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      263
                                                                                                                                                                                                                                                                                                                                                            update:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98;
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                                                                         haemolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7004).
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Qy
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Y765_HAEIN
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                 Q57125; O05033;
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
15-JUN-2002 (Rel. 4
McKenney K.,
Scott J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
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J. Bacteriol. 173:5597-5603(1991).

-i- FUNCTION: INVOLVED IN THE BIOSYNTHESIS

OF THE LIPOPOLYSACCHARIDE MOLECULE.

-i- SUBCELLULAR LOCATION: CYTOPLASMIC. ASSE
                                                                                                                                                                        Hypothetical HI0765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; 1FRVV2003, ---
Pfam; PF01755; Glyco_transf_25; 1.
Pfam; PF01755; Glyco_transf_25; 1.
Pfam; PF01755; Glyco_transf_25; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
 Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick Kerlavage A.K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
                                                STRAIN=Rd / KWZU / AICC JIJV',
MEDLINE=95350630; PubMed=7542800;
                                                                                                                             Bacteria; P:
Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lipopolysaccharide SEQUENCE 263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF THE CYTOPLASMIC MEMBRANE (POTENTIAL).
-I- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 189-
STRAIN=Serotype
                                                                                    SEQUENCE FROM
                                                                                                               NCBI_TaxID=727;
                                                                                                                                                         Haemophilus
                                                                                                                                                                                                                                                          Y765_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U15958; AAA80283.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *Cloning, nucleotide sequence, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Abdullah K.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91358346;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Ew European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LETMFAKVIVRPDKVLNY-ENRSFPLLESEHCGTAGYIISREAMRFFLDRFAVLPPERIK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEKACFMSHAVLWEQALDEGLPYIAVFEDDVLLGEGAEQFLAEDTWLEERFDKDSAFIVR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MNNYVISLTSAQERRKHIEAEFGKQNIPFQFFDAITPDLIKEKAKAFNID--ISNTNLTK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MQNHVISLASAAERRAHIADTFGSRGIPFQFFDALMPSERLEQAMAELVPGLSAHPYLSG
                                                                                                                                                                                                                                                                                                                               KNQAKLKKPNYFLTKIQKELYRPFKQLKQ----
                                                                                                                                                                                                                                                                                                                                                        KVMFDLKRA----LGKFGREKKKRMERQRQAELEKVYGRRVILFK
                                                                                                                                                                                                                                                                                                                                                                                                               AVDLMMFTYFFDKEGMPVYQVSPALCTQELHYAKFLSQNSMLGSDLEKDREQGRRHRRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEIACALSHIALWHLAKQQNLDYICIFEDDIYLGNNAFEL----
                                                                                                                                                                                                                                                                                                                                                                                     IDDLIFDEYLKIKE-YKVLQMSPALCVQDF----ILNSKTNFKSSLQDDRAIRCNNEDKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF 189-263 FROM
                                                                                                                                           Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR002654; GT_25
                                                                                                                                                                                 7 (Rel. 35, Created)
7 (Rel. 35, Last sequence
2 (Rel. 41, Last annotati
11 glycosyl transferase F
                                                                                                                                                         influenzae
                                                                      NM N.A.
KW20 / ATCC 51907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lo R.Y.C.,
                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A1;
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30871 MW; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.0%;
                                                                                                                                                                                                 Last sequence up
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                                                                                                                                           gamma subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 331.5; DB Pred. No. 9e-21; 1; Mismatches 1
                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s; Transferase; Glycosyltransferase
B07C39EC1DA603A7 CRC64;
                                                                                                                                                                                  cion update)
HI0765 (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression
                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                          282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118;
                                                                                                                                         Pasteurellaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usage
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RESULT 10
LSG4_HAEIN
ID LSG4_H
AC P7130-MAY
DT 30-MAY
DT 15-JUN
DE LSG 100
GN H11697
OS Haemopi
OC Haemopi
OX NCBI_T:
RN [1]
RP SEQUEN
RC STRAIN
RA MCLAUGI
RT "Charaa
RT "Charaa
RT "Charaa
RT Influe
RP SEQUEN
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Best Local S
Matches 82
                                                                                                                                                                                                                                                                                                                                                                                    LSG4_HAEIN STANDARD; PRT; 257 AA p71398; Q48213; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat. LSG locus putative protein 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Gnehm C.L., McDonald L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Weidman J.F., Ph
Utterback T.R.,
                                                         Submitted
                                                                                                                                                                      STRAIN-A2;
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Pfam; PF01755; Glyco_transf_25; 1.
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                                                                                   "Characterization influenzae.";
                                                                                                                                         McLaughlin R.,
                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             Haemophilus
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                                                         EMBL/GenBank/DDBJ databases
                                                                                                                                      Young
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Pred. No. 2
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RESULT 11
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            30-MAY-2000 (Rel.
30-MAY-2000 (Rel.
16-OCT-2001 (Rel.
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EMBL; M94855; AAA24981.1;
TIGR; HI1697; -
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39, Last sequence 40, Last annotation
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sequence update)
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51; Mismatches
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Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000766; AAC07746.1; -. HSSP; Q56232; 1BKG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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-!- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate
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InterPro; IPR004839; Aminotransf1/2.
InterPro; IPR004838; NHtransf_1.
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                                                                        FVNEMRNAFERRRDTAVEELSKIPGMDVV
                                                                                                                                                             GMPVYQVSPALCTQELHYAKFL-SQNSMLGSDLEKDREQGRRHRRSLKVMFDLKRALGK-
                                                                                                                                                                                                                                                                                                                                        LMPSERLEQAMAELVPGLSAHPYLSGVEKACFMSHAVLWEQALDEG-----LPYIAVFE 88
                                                                                                                                                                                                                                                                                                                                                                      AKAKELRAKGVDVIGFGAGEPDFDTPDFIKEACIRALREGKTKYAPSAGIPELREAIAEK 81
                                                                                                                                                                                                                                                                                                                                                                                                   ASAAERRAHIADTFG-----
                                                                                                    FGREKKKRMERQRQA---
                                                                                                                               SMTGWRIGYVACPEE--YAKVIASLNSQSVSNVTTFAQYG-----ALEALKNPKSKD
                                                                                                                                                                                          EEEELKKI-AEFCVERGIFIISDECYEYFVYGDAKFVSPASFSDEVKNITFTVNAFSKSY
                                                                                                                                                                                                                      ENRSFPLLESEHCGTAG-YIISREAMRFFL--DRFAVLPPERIKAVDLMMFTY--FFDKE
                                                                                                                                                                                                                                                 EQIRFFGGVP-----VEVPLKKEKGFQLSLEDVKEKVTERTKAIVINSPNNPTGAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 AA; 43777 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                         6.9%;
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                                                                                                    ELEKVYGRRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHATE (BY SIMILARITY).
TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                            ---AGAKMVLFL----IFMAILDEGDEVLLPSPYWVTYP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                38;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 99;
Pred. No.
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E570B4FD080C56E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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   ΑA
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Matches 51
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
[Protein-PII] uridylyltransferase (EC 2.7.7.59)
transferase) (Uridylyl removing enzyme) (UTase)
GLND OR MLL5321.
                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01842; ACT; 2.
Pfam; PF01966; HD; 1.
Pfam; PF01909; NTP_transf_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP003006; BAB51794.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S.,
Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhizobium
                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                              Transferase; Nucleotidyltransferase; Nitrogen fixation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (glnB) regulatory protein.
-!- CATALYTIC ACTIVITY: UTP + [protein-PII]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Res. 7:331-338(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21082930; PubMed=11214968;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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406
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nes 51; Conser
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                                                                                                   MFAKVIVRPDKV-LNYENRSFPLLESEHCGTAGYIISREAMRFFLDRFAVLPPERIKAVD 182
                                                                                                                                                                                                                        HVISLASAAERRAHIADTFGSRGIPFQFFDALMPSERLEQAMAELVPGLSAHPYLSGVEK 63
 LLRLFWFADKHGLEFHPDALKLLTRSL-
                                                                                                                                                                     ACFMSHAVLWEQALDEGLPYIAVFEDDVLLGEGAEQFLAEDTWLEERFDKDSAFIVRLET 123
                                                                                                                                                                                                       HMHFLTGKAEERLH------FD----IQREIAERL-GYTTHPGLSAVER 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein-PII]
                               LMMFTYFFDKEGMPVYQVSPALCTQELHYAKFLSQNSMLGSDLEKDREQGR
                                                                 EQAKHVPGFNRIFLTFQRRKRKL-----AGTSDFIVDNHRINIADDQVFERDP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR002912; ACT.
IPR002819; HD.
IPR003607; ME_Pplase_HDc.
IPR002934; NTP_transf.
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                                                                                                                                                                                                                                                                                                                                              933 AA;
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                               HDc;
                                                                                                                                                                                                                                                                                                                                            105279 MW;
                                                                                                                                                                                                                                                                        6.6%; Score 95.5; D
22.1%; Pred. No. 2.6;
tive 31; Mismatches
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                                                                                                                                     YFLVAKD --- VG
                                                                                                                                                                                                                                                                                                                                            79BF065DAC796FF8 CRC64;
 -GLVNKSLRRDEEANR
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                                                                                                                                                                                                                                                                          72;
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                                                                                                                                                                                                                                                                                                        Length
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RESULT 13 SAD1_MOUSE

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Best Local :
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SMART; SM0045*, SAn_
PROSITE; PS50105; SAn_
Interferon induction.
Interferon 46 111 SAM.
165 320 HD.
165 320 HD.
17 NA; 72650 MW; C
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SAMHD1 OR MG11.

Mis much
                                                                                                                                                                                                                                                                                                Pfam; PF00536; SAM; 1.
Pfam; PF01966; HD; 1.
SMART; SM00471; HDc; 1.
SMART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- INDUCTION: By interferon gamma.
-!- SIMILARITY: CONTAINS 1 SAM DOWAIN.
-!- SIMILARITY: CONTAINS 1 DOWALN.
-!- SIMILARITY: CONTAINS 1 DOWALN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003607; ME_Pplase_HDc.
InterPro; IPR001660; SAM.
                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002819; HD.
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U15635; AAA66219.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     binding protein."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lafuse W.P., Brown D., Castle L., Zwilling "Cloning and characterization of a novel c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Macrophage;
MEDLINE=95190404; PubMed=7884320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAD1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   induced in mouse peritoneal macrophages
  217
                                                     167
                                                                                219
                                                                                                       107
                                                                                                                                174
                             255
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                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAUTION: Ref.1 sequence differs from that shown due to frameshift in position 576. \,
                                                                                                                                                                                                                                                                                                                                                                                        MGI:1927468; Samhdl.
QNSMLGSDLEK-DREQGRRHRRSLKVMFDLKRALGKFGREKKKRMERQRQAELEKVYGRR
                          MKNYGLVPEEDIT-----FIKEQIMGPPITPVKDSLWPYKGRPATKSFLYE--IV
                                                 LDRFAVLPPERIKAVDLMMFTYFFDKE---GMPVYQVSPAL-----CTQELHYAKFLS
                                                                             -----DGRFIPR-----ARPEKKWKHEQGSIEMFE
                                                                                                    LEERFDKDSAFIVRLETMFAKVIVRPDKVLNYENRSFPLLESEHCGTAGYIISREAMRFF 166
                                                                                                                             YLAG----CLV-----RALAEKQPELQISERDILCVQIAGLCHDLGHGPFSHMF----
                                                                                                                                                       YLSGVEKACFMSHAVLWEQALDEGLPYIAVFEDDVL------LGEGAEQFLAEDTW 106
                                                                                                                                                                                                                                                                                                                                                                                                    BC012721; AAH12721.1;
                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 41, Last sequence up (Rel. 41, Last annotation
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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Rodentia;
                                                                                                                                                                                          6.2%;
22.4%;
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                                                                                                                                                                                              Score 89.5;
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HD.
; C68BB653C3F4B17C CRC64;
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Sciurognathi;
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thi; Muridae; Murinae; Mus
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cDNA that is IFN-gamma-
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                                                                                                                                                                                                          DB 1; Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as its content
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RESULT 14
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Best Local
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MEDITAB-87112952; PubMed=3027382;
Bando H., Kusuda J., Gojobori T., Maruyama T., Kawase Bando H., Kusuda J., Gojobori T., Maruyama T., Kawase Torganization and nucleotide sequence of a densovirus host-dependent evolution of the parvoviruses.";
J. Virol. 61:553-560(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1988 (Rel. 09, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Putative noncapsid protein NS-1 (Nonstructural protein NS1) (NO Bombyx densonucleosis virus (BmDNV) (Silkworm densovirus).
Viruses; ssDNA viruses; Parvoviridae; Densovirinae; Iteravirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001257; Parvo_NS1.
Pfam; PF01057; Parvo_NS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M15123; AAA67698.1; -. PIR; C26796; VCPVF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VNCS_BMDNV
P05842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nonstructural
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DSRIALGELQKQRKMNL
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                                                                                                                                                                                                                                                                                                                                                            HIADTFGSRGIPFQFFDALMPSERLEQAMAELVPGLSAHPYLSGVEKACFMSHAVLWEQA
                                                                                                                               ASNNLNAFVDYMGYNYFGEQKAPQSMPKFMIGFVNIRNE-
                                                                                                                                                                                                                                                             VDYSLPY---FENNVPKDVGIYDYVDIKNGTTAYGKCWEKRFKPTNGLLYAESTLKGNVV
                                                                                                                                                                                                                                                                                             LDEGLPYIAVFEDDVLLGEGAEQFL-----AEDTWLEERFDKDSAFIVRLETMFAKVI 129
                                                                KTRIRLTGLQSTREWVARTDRIPPQYFTSQYTQFRYPNINDTPLLRSLGTFKLPTKRPGM
                                                                                                                                                               -----VDLMMFTYFFDK---EGMPVYQVSPALCTQELHYAKFLSQNSMLG------
                                                                                                                                                                                                TPLAAPTNIMT - - - - PIPGLEN - - - -
                                                                                                                                                                                                                              ---VRPDKVLNYENRSFPLLESEHCGTAGYIISREAMRFFLDRFAVLPPERIKA-----
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 88.5;
Pred. No. 9
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Best Local Similarity
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InterPro; IPROUZ4±1, --
Pfam; PF00010; HLH; 1.
Pfam; PF01056; Myc_N_term; 1.
Pfam; PR01056; Myc_N_term; 1.
PRINTS; PR00044; LEUZIPPRMYC.
SMART; SM00353; HLH; 1.
PROSITE; PS00038; HLH_1; 1.
PROSITE; PS00038; HLH_2; 1.
Nuclear protein; DNA-binding; Proto-oncogene; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M29069; AAA41645.1; -.
PIR; A36220; A36220.
HSSP; P25912; 1HLO.
TRANSFAC; T03550; -.
InterPro; IPR001092; HLH_basic.
InterPro; IPR002418; TF_Myc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene family.";

Proc. Natl. Acad. Sci. U.S.A. 86:9144-9148(1989).
-!- FUNCTION: HAS A SUPPRESSIVE EFFECT ON TUMORIGENICITY (IN VITRO).
-!- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Nishimura S., Kuchino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90083224;
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                                144 PLLESEHCGTAGYIISREAMRFFLDRFAVLPPERIKAVDLMMFTYFFDKEGMPVYQ---- 199
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                                                                                                                                                                                                                                                                                                                                                                            DIFGLKGLSGSSSNPVVLQDCMWSGFSSREKPETVVSEKLPGGCGSLAVGAGTLVPGAAA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                             DTFGSRGI-----PFQFFDALMPS----ERLEQAMAE-----LVPGLSA 54
                                                                                                                                                                                                                                        ATSAGHARSGTAGVGRRKAAWLTELSHLDSEC-VDSAVIFPANKRESMPVATIPASAGAA 215
                                                                                                ISLGDHQGLSSSLEDFLSNSGYVEE--GGEEIYVVMLGETQFSKTVTKLPTAAHSENAAL 273
                                                                                                                                                                    --FEDDVLLGEGAEQFLAEDTWLEERFDKDSAFIVRL-ETMFAKVIVRPDKVLNYENRSF 143
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1E79FF90747FD0FA CRC64;
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Search completed: December 2, 2002, 11:56:31
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel:
9: sp_phage:*.
10: sp_plant:*
11: sp_rodent:*
11: sp_rotent:*
12: sp_virus:*
13: sp_verteb:*
14: sp_unclass:
15: sp_roteris:
16: sp_bacteris:
16: sp_bacteris:
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Match
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Copyright (c) 1993 - 2002 Compugen Ltd.
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116
 Q93PR7
Q92PVD3
Q93EK4
Q93PR9
Q93EK5
Q92FM6
Q92FPB4
Q92FPB4
Q92FPB4
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Ogrex4 neisseria g

Ogrgm8 neisseria m

P96947 neisseria m

Ogspr7 neisseria m

Ogsek4 neisseria m

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Ogsek5 neisseria m

Ogsek5 neisseria m

Ogrgn1 neisseria s

Ogerku0 haemophilus

Ogel18 haemophilus

Ogel18 haemophilus

Ogel18 pasteurella

Ogel26 rhizobium 1
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95.5	96.5	97	97	97	97	97.5	98.5	99	99.5	102	104	109	111	111	112	120.5	121	124.5	125.5	128.5	129.5	131	134	134	139	144	171.5	233
6.6	6.7	6.7	6.7	6.7	6.7		6.8	6.9	6.9	7.1	7.2	7.6	7.7	7.7	7.8	8.4	8.4	8.6	8.7	8.9	9.0	9.1	9.3	9.3	9.7	10.0	11.9	16.2
575	257	1446	839	444	273	224	721	273	287	224	273	261	243	231	254	332	738	261	207	517	560	247	257	251	230	1128	242	268
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Q9ka17 bacillus ha	Q9alt2 campylobact	Q9svt9 arabidopsis	Q9m0g3 arabidopsis	Q9z116 helicobacte	Q9rhg8 helicobacte	Q47960 haemophilus	Q8yg36 brucella me	Q9z117 helicobacte	006023 haemophilus	Q9x6q5 actinobacil	O25500 helicobacte	Q9cnc3 pasteurella	Q9h6f1 homo sapien	Q8wui9 homo sapien	Q9alz3 campylobact	Q9z117 helicobacte		-			Q9p226 homo sapien	Q48023 haemophilus		Q9aly2 campylobact		Q9vmq6 drosophila	Q8rjk5 vibrio chol	Q8yim5 brucella me

ALIGNMENTS

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7 121 LETMFAKVIVRÞÓKVLNYENRSFÞLLESEHCGTAGYTISREAMRFFLDRFAVLÞÞERIKA 180 	61 VEKACEMSHAVLWEQALDEGLPYIAVFEDDVLLGEGAEQFLAEDTWLEERFDKDSAFIVR 120 	1 MQNHVISLASAAERRAHIADTFGSRGIPFQFFDALMPSERLEQAMAELVPGLSAHPYLSG 60 	Query Match 99.7%; Score 1436; DB 2; Length 280; Best Local Similarity 99.6%; Pred. No. 1.2e-119; Matches 279; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	<pre></pre>			gonococci.";	"Mutations in the lgt operon	Ralthazar I T., Shafer W.M., Stephens D.S., Martin L.E.;			NCBI_TaxID=485;) Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.	LGTE.		01-MAR-2002 (TrEMBLrel. 20,	01-MAY-2000 (TrEMBLrel. 13,	01-MAY-2000 (TremBirel. 13, Created)		NESOLI: I	1

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Matches 266
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P96947;
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01-MAY-1997 (TrEMBLrel. C
01-MAR-2002 (TrEMBLrel. C
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01-MAY-2000
01-MAY-2000
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Bacteria;
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Bacteria; Proteobacteria;
                                       Neisseria meningitidis.
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                 Proteobacteria;
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Pred. No. 1.
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                 subdivision;
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01-DEC-2001 (TrEMBLrel. 19, C

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01-MAR 2002 (TrEMBLrel. 20, I

01'000svl transferase LgtE.
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                                                                                                                                                                                                                                                                                                                          Tong Y., Arking D., Reinhold V., Stein D.C.;
"Characterization of lipooligosaccharide structures found
gonorrhoeae PID2.";
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Pfam; PF01755; Glyco_transf_25;
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"The genetic basis of the phase variation
                                                                                                                                                                                    Transferase
SEQUENCE :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria gonorrhoeae
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InterPro; IPR002654; GT_25.
Pfam; PF01755; Glyco_transf_25;
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93.6%;
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                                                                                        Score 1344; DB 2;
Pred. No. 1.9e-111;
5; Mismatches 13;
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Pred. No. 1.5e-111;
8; Mismatches 10;
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in Neisseria meningitidis
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RESULT
Q93EK4
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Best Local S
Matches 253
 Q93EK4;
01-DEC-2001
01-DEC-2001
                                 Q93EK4
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01-MAR-2001
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"Analysis of lipooligosaccharide biosynthesis
J. Bacteriol. 183:934-941(2001).
EMBL; AF246672; AAG09766.1; -
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Bacteria; Proteobacteria;
NCBI_TaxID=28449;
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PF01755; Glyco_transf_25; 1.
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                                 PRELIMINARY;
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No. 2.2e-106;
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RESULT 7
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DF 01-F
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  Query Match
Best Local Similarity
Matches 214; Conser
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Best Local
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Q93PR9;
Q1-DEC-2001 (TrEMBLrel. 19, C)
Q1-DEC-2001 (TrEMBLrel. 19, I)
Q1-MAR-2002 (TrEMBLrel. 20, I)
G1ycosyl transferase LgtB.
                                                                                                                    Tong Y., Arking D., Reinhold V., Stein D.C.; "Characterization of lipooligosaccharide struc gonorrhoeae PID2."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ EMBL; AF313394; AAK70339.1; -. InterPro; IPR002654; GT_25. Pfam; PF01755; Glyco_transf_25; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      LGTB.
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Bacteria;
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Bacteria; Proteobacteria;
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Zhu P., Klutch M.J., Tsai C.-M.;
"Genetic Analysis of Conservation and Variation of Lipooligosaccharide Expression in Two L8-Immunotype Strains of Neisseria meningitidis.";
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                                                                                   Transferase.
SEQUENCE 279
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EMBL; AF355193; AAL12842.1; -.
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PF01755; Glyco_transf_25;
NCE 280 AA; 32898 MW; 5
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Proteobacteria;
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9; Mismatches
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                     Score 1046.5;
Pred. No. 5.16
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structures
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Q1-DEC-2001
Q1-MAR-2002
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"Genetic Analysis of Conservation and Variation of Lipooligosaccharide Expression in Two L8-Immunotype Strains of Neisseria meningitidis.";

FEMS Microbiol. Lett. 203:173-177(2001).

EMBL; AF355193; AAL12841.;

InterPro; IPR002654; GT_25.

Pfam; PF01755; Glyco_transf_25; 1.

SEQUENCE 275'AA; 31577 MW; A73037E0625EE7B3 CRC64;
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Q9JW65;
01-OCT-2000
01-OCT-2000
01-MAR-2002
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MEDLINE-21467954; PubMed-11883844;
Zhu P., Klutch M.J., Tsai C.-M.;
"Genetic Analysis of Conservation and Variation of Lipooligosaccharide
"Genetic Analysis of Conservation and Variation of Lipooligosaccharide
Expression in Two L8-Immunotype Strains of Neisseria meningitidis.";
FEMS Microbiol. Lett. 203:173-177(2001).
EMBL; AL162753; CAB83819.1; -.
EMBL; AF355194; AAL12844.1; -.
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SPECIES=N.meningitidis (serogroup A);
STRAIN=Z3491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE=20222556; PubMed=10761919;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Lacto-N-neotetraose biosynthesis glycosyl tranferase
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PF01755; Glyco_transf_25;
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Pred. No. 1.6e
24; Mismatches
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.6e-81;
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Q9RGN1; Q9RGN1; 01-MAY-2000 01-MAY-2000 01-MAR-2002

PRELIMINARY

PRT;

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Glycosyltransferase

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Best Local Sim
Matches 194;
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Best Local Similarity
Matches 198; Conser
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01-MAR-2001
01-MAR-2001
01-MAR-2002
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Pfam; PF01755; Glyco_transf_25; 1.
Transferase.
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Pfam; PF01755; Glyco_transf_25; 1.
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Arking D., Tong Y., Stein D.C.;
"Analysis of lipooligosaccharide biosynthesis
J. Bacteriol. 183:934-941(2001).
EMBL; AF240672; AAG09765.1; -.
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Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria;
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EMBL; AF121135; AAF14360.1; -.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20305049; PubMed=10844691;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEKACFMSHAVLWEQALDEGLPYIAVFEDDVLLGEGAEQFLAEDTWLEERFDKDSAFIVR 120
VEKACFMSHAVLWEQALDEGLPYIAVFEDDVLLGEGAEQFLAEDTWLEERFDKDSAFIVR
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                                    MQNHVISLASAAERRAHITDTFGVRGIPFQFFDALMPSERLEQVMAELVPGLSAHPYLSG
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Proteobacteria;
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Last sequence update)
Last annotation updat
                                                                                                           Score 984; DB 2;
Pred. No. 1.8e-79;
1; Mismatches 46
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Pred. No. 4.9e-81;
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RESULT 13
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Best Local
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Q9L7A4;
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
Galactosyltransferase
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SEQUENCE
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"Identification of LOS biosynthesis gen
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01-MAY-1999 (TrEMBLr:
01-MAY-1999 (TrEMBLr:
01-MAR-2002 (TrEMBLr:
01-Glycosyltransferase)
                                                               Transferase.
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Munson R.S. Jr.;
"Cloning and characterization of the lipooligosaccharide galactosyltransferase II gene of Haemophilus ducreyi.";
J. Bacteriol. 18::2297-2298(2000).
                                                                                                                                                                                           MEDLINE=20072700; PubMed=10603403; Wu Y., McQuiston J.H., Cox A., Pack T.D., Inzana T.J.; "Molecular cloning and mutagenesis of a DNA locus involventipooligosaccharide biosynthesis in Haemophilus somnus."; Infect. Immun. 68:310-319(2000).
EMBL, AF095997; AAC83803.1; -.
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Haemophilus
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Pfam; PF01755; Glyco_transf_25;
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                                                                                                                              PF01755;
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                                                                                                                           96997; AAC83803.1; -.
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B., Tarantino L.,
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Pred. No. 1.3e-31;
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Matches 85
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Q9CLR8;
Q1-JUN-2001
01-JUN-2001
01-MAR-2002
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MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.:
"Complete genomic sequence of Pasteurella multocida Pm"
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

EMBL; AE006155; AAK03225.1; -.
InterPro; IPR002654; GT_25.
Pfam; PF017755; Glyoc_transf_25; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 208 AA; 24649 MW; 29625BAll5E4047A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical PM1141.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pasteurella
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                                                                                                                                                                                                                                                                                                                                                       LWEQALDEGLPYIAVFEDDVLLGEGAEQFLAEDTWLEERFDKDSAFIVRLETMFAKVIVR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MQNHVISLASAAERRAHIADTFGSRGIPFQFFDALMPSERLEQAMAELVPGLSAHPYLSG
-KKTWREKVYHIFTKPQRMLKKRKERAEK
                                                                                                LAGEELMVYQLSPALCIQELQ----LNENESLLDSQLESERKNYRLAEKARK--
                                                                                                                                FDKEGMPYYQVSPALCTQELHYAKFLSQN-SMLGSDLEKDREQGRRHRRSLKVMFDLKRA
                                                                                                                                                                                                      ALPNPV-SYCGRDFLALKDEHLGTAGYIISLGAAKYLLEIFKNMESNNIFPIDHLIFNRF
                                                                                                                                                                                                                                                    --PDKVLNYENRSFPLLESEHCGTAGYIISREAMRFFLDRFAVLPPERIKAVDLMMFTYF 189
                                                                                                                                                                                                                                                                                                         MWHKCIQDNLPYIAIFEDDILLGRDARTFLAEDEWLFSRFNCDDIFIIRLETFLQETICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEKACEMSHAVLWEQALDEGLPYIAVFEDDVLLGEGAEQFLAEDTWLEERFDKDSAFIVR 120
                                                  LGKFGRE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RERESKNIKKAKKILWRSISKEIGRFRRRIFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REQGRRHRRSLKVMFDLKRALGK-FGREKKKRMER 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LETMFAKVIVRPDKVLNYENRSFPLLESEHCGTAGYIISREAMRFFL-----DRFAVLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LETIYMKSEYCKTKIPDYQNRKFNRLMSGHFGMGGYILSQVAAKKLLALFKNTDIF----
                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 17, (TrEMBLrel. 17, CTEMBLrel. 20, CTEM
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                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein PM1141
                             KKKRMERQRQAELEK
                                                                                                                                                                                                                                                                                                                                                                                                          24.4%; Score 351; DI
40.7%; Pred. No. 2.30
tive 32; Mismatches
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5; Mismatches
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  195
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No. 2.3e-23;
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les 101;
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